Thu Jun 24

08:47:52 2004

## epper526106.pep.rapm

04/526106 Page 1 567.107 (C) (8)

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OM protein -
                                                  Run on:
                                                                                             protein search, using sw model
June 18, 2004, 19:08:03; Search time 184 Seconds (without alignments)
1395.120 Million cell updates/sec
                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Title: Perfect score: Total number of hits satisfying chosen parameters: Searched: Scoring table: Sequence: 1 hpetlvkvkdaedqlgarvg.....tmdernrqiaeigaslikhw 263 6019581 seqs, 976053577 residues Gapop 10.0 , Gapext 0.5 BLOSUM62 EPPER526106.PEP 1345 6019581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

18: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep:\*
/cgn2\_6/ptodata/2/paa/US080\_COMB.pep:\*
/cgn2\_6/ptodata/2/paa/US081\_COMB.pep:\*
/cgn2\_6/ptodata/2/paa/US082\_COMB.pep:\*
/cgn2\_6/ptodata/2/paa/US083\_COMB.pep:\*
/cgn2\_6/ptodata/2/paa/US086\_COMB.pep:\*
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/cgn2\_6/ptodata/2/paa/US103\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed,

## SUMMARIES

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	eque	quence 9,	equence 2, Appli	equence 300,	equence 2	equence 285,	equence 300,	equence 298,	equence 285,	equence 300,	equence 298,	equence 28	e 11955	equence 11955,	equence 1215,	equence 11955,	12	equence 4	equence 3	equence 3	equence 2	equence 1	equence 7	equence 5	equence 4	equence 4	equence 3	equence 1	equence 3	equence 2	equence 3	ddy yyc apmandas ddy yyc apmandas	equence 2	equence 2	equence 1	equence 7	equence 21	equence 14	nce 7,	equence 52	equence 2	quence 9	equence 2, A	, Appl

## ALIGNMENTS

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Sequence 2, Application US/09526106; GENERAL INFORMATION:

APPLICANT: Balint, Robert F.

APPLICANT: Her, Jeng-Horng
APPLICANT: KaloBios, Inc.

TITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/09/526,106
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/135,926
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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US-09-526-106-2
                        LENGTH: 263
TYPE: PRT
ORGANISM: Escherichia coli
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; Sequence 2, Application US/09764163A
.; GENERAL INFORMATION:

; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
APPLICANT: KaloBios, Inc.
TITLE OF INVENTION: Circularly Permutated, In
FILE REFERENCE: 021167-000710US
CURRENT APPLICATION NUMBER: US/09/764,163A
CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: US 09/526,106
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
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; OTHER INFORMATION: TEM-1 beta-lactamase US-09-526-106-2
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Matches 260; Conserv
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Pred. No. 5.2e-132;
1; Mismatches 2;
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APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: PatentIn version 3.0

SEQ ID NO 90233

LENGTH: 263
                                            Sequence 2, Application US/10668778

GENERAL INFORMATION:

APPLICANT: Balint, Robert F.

APPLICANT: Her, Jeng-Horng

APPLICANT: KaloBios, Inc.

TITLE OF INVENTION: Interaction-Activated Properties

CURRENT APPLICATION NUMBER: US/10/668,778

CURRENT FILING DATE: 2003-09-22

PRIOR APPLICATION NUMBER: US/09/526,106

PRIOR FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 60/124,339

PRIOR FILING DATE: 1999-03-15

PRIOR APPLICATION NUMBER: US 60/135,926

PRIOR APPLICATION NUMBER: US 60/135,926

PRIOR APPLICATION NUMBER: US 60/175,968

PRIOR APPLICATION NUMBER: US 60/175,968

PRIOR FILING DATE: 2000-01-13
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Best Local Similarity 98.9%;
Matches 260; Conservative
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
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Pred. No. 5.2e-132;
1; Mismatches 2;
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APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: PCT/US02/12405
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
SEQ ID NO 523
LENGTH: 286
TYPE: PRT

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Best Local
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Best Local Similarity
Matches 260; Conserv
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                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Escherichia
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EDWARD H.
HORACIO G.
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1; Mismatches
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Pred. No. 5.2e-132;
Pred. No. 5.2e-132;
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                                                                                                                                         e 1330; DB 1; L
. No. 6e-132;
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RESULT 6
PCT-US99-17440-7
; Sequence 7, Application PC/TUS9917440
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HEPA
; TITLE APPLICATION NUMBER: PCT/US99/17440
; CURRENT APPLICATION NUMBER: PCT/US99/17440
; CURRENT FILING DATE: 1999-08-02
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; Sequence 14, Application PC/TUS99174; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SY
; TITLE OF INVENTION: OF INHIBITORS OF FILE REFERENCE: 0125-0005A
                                                                                                                  RESULT 7
PCT-US99-17440-14
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↑ RESULT 8

PCT-US99-17440-21

; Sequence 21, Application PC/TUS9917440
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HEPA'
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: PCT/US99/17440
; CURRENT FILING DATE: 1999-08-02
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; Type. Der
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CURRENT FILING DATE: 1999-08-02
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
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KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLIGELLTLASRQ
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nilarity 98.9%;
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Pred. No. 6e-1
1; Mismatches
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Pred. No. 6e-132;
1; Mismatches
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RESULT 10

US-09-129-611-14

; Sequence 14, Application US/09129611A
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR
TITLE OF INVENTION: OF INHIBITORS OF THE HEPA
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/129,611A
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
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US-09-129-611-7
; Sequence 7, Applicat
; GENERAL INFORMATION:
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR
TITLE OF INVENTION: OF INHIBITORS OF THE HEPA
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/129,611A
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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SEQ ID NO 7
LENGTH: 286
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Best Local Similarity
Matches 260; Conserv
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ORGANISM: Artificial
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Pred. No. 6e-132;
1; Mismatches 2;
                                                                                                           SYSTEM FOR USE
OF THE HEPATITI
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HEPA FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/129,611A

CURRENT FILING DATE: 1999-08-05

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

COSTWARD. Date: 1998-08-05
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; TYPE: PRT
; ORGANISM: Artificial
US-09-129-611-14
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ORGANISM: Artificial Sequence
-09-129-611-21
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                                                                                                                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                              HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID
                 QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                        AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                          KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRO
                                                                               KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ
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 QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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larity 98.9%;
Conservative
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Pred. No. 6e-132;
1; Mismatches 2;
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C VIRUS PROTEASE
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: pC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EP
CURRENT APPLICATION NUMBER: US/09/490,070
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: 09/025,769
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
                                                                                                                                                                                                                                                                                                                  ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ
US-09-490-070-265
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US-09-490-070-265
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; GENERAL INFORMATION:
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Best Local Similarity
Matches 260; Conserv
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Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Po
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ADDRESSEE: James F.
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SQATMDERNRQIAEIGASLIKHW 263
                                              OLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPI
                                                                                                    KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
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STATE: New York
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nilarity 98.9%;
Conservative
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Moroney, Simon
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Pred. No. 6e-132;
1; Mismatches
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                            DGKPSRIVVIYTTG 240
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SQATMDERNRQIAEIGASLIKHW 286

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RESULT 13
US-09-490-070-362
; Sequence 362, Application
; GENERAL INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070-362
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: 09/025,769
FILING DATE: <Unknown>
APPLICATION NUMBER: 07.759
FILING DATE: <Unknown>
APPLICATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 362:
SECUTEMER CHARBOTERICS.
                                                                                                                                                                                                                                                                                                                                 Query Match 98.9%;
Best Local Similarity 98.9%;
Matches 260; Conservative
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ADDRESSEE: James F.
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Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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                        SQATMDERNRQIAEIGASLIKHW 263
                                                                                                                                  KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 286 amino acids TYPE: amino acid
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                                                                                               QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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Ilag, Vic
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Pred. No. 6e-132;
l; Mismatches 2;
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US-09-490-070A-265
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Versic
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
FENCTH: 286 amino acids
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APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.9%;
Best Local Similarity 98.9%;
Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 265:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                               181
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                                                                                                OLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240
                                                                                                                                                                                                                             AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTTIGGP 143
                                                                                                                                                                                                                                                AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
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STATE: D.C.
COUNTRY: USA
                                   SQATMDERNRQIAEIGASLIKHW 263
                                                                                                                                                    KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERD
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White & McAuliffe
STREET: 1666 K Street, N.W., Su:
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Pack, Peter
Ilag, Vic
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Pred. No. 6e-132;
1; Mismatches 2;
286
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RESULT 15
US-09-490-070A-362
; Sequence 362, Application US/09490070A
; GENERAL INFORMATION:
: APPLICANT: Knappik, Achim
Pack, Peter
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 362:
US-09-490-070A-362
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELEPHONE: (202) 912-2020
INFORMATION FOR SEQ ID NO: 362:
SECURENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.9%;
Best Local Similarity 98.9%;
Matches 260; Conservative
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Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
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ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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LENGTH: 286 amino acids
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                                                                                          QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                          KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                             SQATMDERNRQIAEIGASLIKHW 263
                                                                                                                                                                                                                       AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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Pred. No. 6e-132;
1; Mismatches 2;
286
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Search completed: June 18, 2004, 19:13:52 Job time : 185 secs

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# epper526106.pep.rsp

Database :	Post-processing: Minimum Match Maximum Match Listing first	Minimum DB seq lo Maximum DB seq lo	Total number of l	Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:	OM protein - pro	
SwissProt_42:*	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	seq length: 0 seq length: 2000000000	Total number of hits satisfying chosen parameters: 141681	141681 seqs, 52070155 residues	BLOSUM62 Gapop 10.0 , Gapext 0.5	EPPER526106.PEP 1345 1 hpetlvkvkdaedqlgarvgtmdernrqiaeigaslikhw 263	June 18, 2004, 18:30:18 ; Search time 18 Seconds (without alignments) 760.803 Million cell updates/sec	- protein search, using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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## ALIGNMENTS

RP RT RT RT	RP RX RA RT RT RL	RC R	RP RT RX RR	RESUI BLAT ID AC DT DT DT DT DE DE OS OS OC OC
SEQUENCE FROM N.A. (TEM-3). Sougakoff W., Goussard S., Courvalin P.; "The TEM-3 beta-lactamase, which hydrolyzes broad-spectrum cephalosporins, is derived from the TEM-2 penicillinase by two amino acid substitutions."; FEMS Microbiol. Lett. 56:343-348(1988).	SEQUENCE OF 24-286 (TEM-2).  SPECIES=E.coli; PLASMID=R6K; TRANSPOSON=Tn1;  MEDLINE=79012483; PubMed=358199;  Ambler R.P., Scott G.K.;  "Partial amino acid sequence of penicillinase coded by Escherichia coli plasmid R6K.";  Proc. Natl. Acad. Sci. U.S.A. 75:3732-3736(1978).	SEQUENCE FROM N.A. (TEM-1).  SPECIES=E.coli; PLASMID=R1 (R7268); TRANSPOSON=Tn3;  MEDLINE=80002802; PubMed=383387;  Sutcliffe J.G.;  "Complete nucleotide sequence of the Escherichia coli plasmid pBR322.";  Cold Spring Harb. Symp. Quant. Biol. 43:77-90(1979).  [3]  SEQUENCE FROM N.A. (TEM-1).  PLASMID=IncFII R100;  MEDLINE=86319522; PubMed=3019092;  Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.;  "DNA replication of the resistance plasmid R100 and its control.";  Adv. Biophys. 21:115-133(1986).	SEQUENCE FROM N.A. (TEM-1). SEQUENCE FROM N.A. (TEM-1). SPECIES=E.coli; PLASMID=R1 (R7268); TRANSPOSON=Tn3; MEDLINE=79012484; PubMed=358200; Sutcliffe J.G.; "Nucleotide sequence of the ampicillin resistance gene of Escherichia coli plasmid pBR322."; Proc. Natl. Acad. Sci. U.S.A. 75:3737-3741(1978). [2]	

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C SPECIES=S.typhi; STRAIN=CT18; PLASMID=pHCM1;

X MEDLINE=21534947; PubMed=11677608;

X Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

A Chircher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

B Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

A Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

A Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

A Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

A Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

A Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,

A Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";

I Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE STRAIN=PEY;
STRAIN=94333751; I
MEDLINE=94333751; I
                                                                                                                 "Beta-lactamase TEM1 o
2.5-A resolution.";
FEBS Lett. 200-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goussard S., Sougakoff W., Mabilat C., Bauernfeind A., Courve "An IS1-like element is responsible for high-level synthesis extended-spectrum beta-lactamase TEM-6 in Enterobacteriaceae. J. Gen. Microbiol. 137:2681-2687(1991).

[9]
SEQUENCE FROM N.A. (MDD)
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MEDLINE=93037315; Pu
Chanal C., Poupart N
"Nucleotide sequence
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the broad-spectrum beta-lactamases TEM-4 and TEM-5 in
enterobacteriaceae.";
Gene 78:339-348(1989).
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SEQUENCE FROM N.A. (TEM-3).
SEQUENCE FROM N.A. (TEM-3).
PLASMID=pCFF04;
MEDLINE=93062798; PubMed=1331747;
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SEQUENCE
resolution. Proteins 16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mabilat C., Lourencao-Vital J., Goussard S., Courvalin P.; "A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple-resistance region of plasmid pCFF04 encoding extended-spectrum beta-lactamase TEM-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme with a inhibitors.";
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MEDLINE=92183921; PubMed=1544485;
Jelsch C., Lenfant F., Masson J.-
"Beta-lactamase TEM1 of E. coli.
                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTR
MEDLINE=93361453; PubMed=8356032;
Jelsch C., Mourey L., Masson J.-M
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                                               structure
                  16:364-383(1993)
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                                                                                                                        299:135-142(1992)
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J., Canica M.M.,
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A93821; PNE S30113; S30

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AAB64386.1; AAC48875.1; 33; CAD09800.1

15-MAY-97. 15-MAY-97. 01-APR-97. 18-NOV-98. 18-AUG-99. 02-SEP-99. 20-DEC-00. 20-DEC-00. 20-DEC-00. 01-NOV-00. 18-DEC-02. 17-OCT-01.

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"X-ray structure of the Asn276Asp variant of the Escherichia coling TEM-1 beta-lactamase: direct observation of electrostatic modulation in resistance to inactivation by clavulanic acid.";

El Biochemistry 38:9570-9576(1999).

C -!- FUNCTION: TEM-type are the most prevalent beta-lactamases in including they hydrolyze the beta-lactam bond in susceptible beta-lactam antibiotics, thus conferring resistance to penicillins include and cephalosporins. TEM-3 and TEM-4 are capable of hydrolyzing cefotaxime and ceftazidime. TEM-5 is capable of hydrolyzing ceftazidime. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly aztreonam. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly active against ceftazidime. IRT-4 shows resistance to beta-including ceftazidime. CaTALYTIC ACTIVITY: A beta-lactam + H(2)0 = a substituted beta-
EMBL; J01749; I

EMBL; X64523; Q

EMBL; X57972; Q

EMBL; X65252; Q

EMBL; X65254; Q

EMBL; X65254; Q

EMBL; X65254; Q

EMBL; U89928; I

EMBL; U89928; I

EMBL; U9928; I

EMBL; U9928; I

EMBL; U56885; I

EMBL; AL513383; Q

PIR; A93821; P

PIR; S30113; S3

PIR; S30113; S3

PIR; S30113; S3

PIR; S30113; S3

PDB; 1BTL; 26-1

PDB; 1ETM; 15-1

PDB; 1XPB; 01-1

PDB; 1XPB; 01-1

PDB; 1ERM; 20-1

PDB; 1ERQ; 20-1

PDB; 1ERQ; 20-1

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MEDLINE=98153145; PubMed=9485412;
Maveyraud L., Pratt R.F., Samama J.-P.;
"Crystal structure of an acylation transition-state
"EM-1 beta-lactamase. Mechanistic implications for clack-interior.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strynadka N.C.J., Jensen S.E., Alzari P. "A potent new mode of beta-lactamase inh X-ray crystallographic structure of the Nat. Struct. Biol. 3:290-297(1996).
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MEDLINE=96186252; PubMed=8605632;
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SIMILARITY: Belongs to the class-A beta-lactamase family.
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BIOTECHNOLOGY: This
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CAA23886.1;
CAA45828.1;
CAA41038.1;
CAA46344.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry is copyright. It is produced throug
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to license@isb-sib.ch)
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PubMed=10423234;
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Best Local
Matches 25
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BLA OR SHV1.
Escherichia coli, and
Klebsiella pneumoniae.
Plasmid R974, and Plasmid p
Bacteria; Proteobacteria; G
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SPECIES=E
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SPECIES=K.pneumoniae; PLASMID=R974;

MEDLINE=91024126; PubMed=2221867;

Mercier J., Levesque R.C.;

"Cloning of SHV-2, OHIO-1, and OXA-6 beta-lactama sequencing of SHV-1 beta-lactamase.";

Antimicrob. Agents Chemother. 34:1577-1583(1990).
Bradford P.A.;
"Automated thermal cycling is superior to trace nucleotide sequencing of blaSHV genes.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ [5]
SEQUENCE OF 22-286.
SPECIES=E.coli; PLASMID=p453;
                                                                                                                                                                                                                                                                                       SPECIES=K.pneumoniae; STRice L.B., Bonafede M., Submitted (JAN-1999) to [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SPECIES=K.pneumoniae; STRAIN=KPAA-1, KPZU-8, and KPZU-
SPECIES=K.pneumoniae; STRAIN=KPAA-1, KPZU-8, and KPZU-
SPECIES=7291235; PubMed=9145849;
Nuesch-Inderbinen M., Kayser F.H., Hachler H.;
"Survey and molecular genetics of SHV beta-lactamases
Enterobacteriaceae in Switzerland: two novel enzymes,
12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid R974, and Plasmid p453.

Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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Coli; STRAIN=HB101;
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                                                                                                                                                                                                                                                                                                           STRAIN=15571;
., Hujer A.M., Bonomo R.l
to the EMBL/GenBank/DDBJ
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t annotation update)
t annotation (EC 3.5.2.6) (F
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Pred. No. 6.6e-98;
2; Mismatches 3;
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CONFLICT HELIX

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X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).

SPECIES=K.pneumoniae; STRAIN=15571;

MEDLINE=99249781; PubMed=10231522;

Kuzin A.P., Nukaga M., Nukaga Y., Hujer A.

"Structure of the SHV-1 beta-lactamase.";

Biochemistry 38:5720-5727(1999).

-!- CATALYTIC ACTIVITY: A beta-lactam + H(
amino acid.

-!- SIMILARITY: BELONGS TO THE CLASS-A BET
IN ONLY ONE POSITION FROM SHV-2.
                                                                                                                                                                                Hydrolase;
SIGNAL
CHAIN
ACT SITE
DISULFID
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InterPro;
Pfam; PF00
PRINTS; PR
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Barthelemy M., Peduzzi
"Complete amino acid s
lactamase (SHV-1).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=E.coli; PLASMID=p453;
MEDLINE=87279638; PubMed=3497152;
Barthelemy M., Peduzzi J., Labia R.;
"N-terminal amino acid sequence of PIT-2 beta-lactamase
"N-terminal amino acid sequence of PIT-2 beta-lactamase
J. Antimicrob. Chemother. 19:839-841(1987).
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IL; X98098; CAA66726.1; -.

IL; X98099; CAA66727.1; -.

IL; X98100; CAA66728.1; -.

IL; AF124984; AAD18054.1; -.

IL; AF148850; AAD37412.1; -.

I; A44996; A44996.
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erPro; IPR000871; Beta lactamase A.
m; PF00144; beta-lactamase; 1.
NTS; PR00118; BLACTAMASEA.
SITE; PS00146; BETA LACTAMASE A; 1.
rolase; Antibiotic resistance; Plasmi
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1G56; 14-FEB-01.
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Peduzzi
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duzzi J., Labia F
cid sequence of F
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G -> A (IN REF. 1).
AT -> TA (IN REF. 5)
KL -> NVG (IN REF. 1).
A -> K (IN REF. 1).
I -> Y (IN REF. 1).
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e; Plasmid;
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Beta-lactamase SHV-
BLA OR SHV13.
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                               MEDLINE=20187177; PubMed=10722518;
Yuan M., Hall L.M.C., Savelkoul P.
                                                                                                           Enterobacteriaceae;
NCBI_TaxID=573;
                                                                                                                                              Bactería;
                                                                                                                                                            Plasmid
                                                                                                                                                                            Klebsiella
                                                                  STRAIN=803;
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                                                                                 FROM
                                                                                                                              Proteobacteria; Gammaproteobacteria; teriaceae; Klebsiella.
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el. 40, Last sequence update)
el. 41, Last annotation update)
SHV-13 precursor (EC 3.5.2.6).
                                                                                                                                                                                                                                                                                        STANDARD;
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   extended-spectrum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 942; DB 1;
Pred. No. 1.5e-67;
3; Mismatches 45
                                                                                                                                                                                                                                                                                          PRT;
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                                  Vandenbroucke-Grauls
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RESULT 4

BLA8 ECOLI

ID BLA8 ECOLI STANDARD;

AC 008337;

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DT 16-OCT-2001 (Rel. 40, Last
DT 16-OCT-2001 (Rel. 40, Last
DT 16-OCT-2001 (Rel. 40, Last
DE Beta-lactamase SHV-8 precur
GN BLA OR SHV8.

OS Escherichia coli.

OC Bacteria; Proteobacteria; G
OC Enterobacteriaceae; Escheri
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BINDING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF164577; AAD43815.1; -.
HSSP; P14557; ISHV.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; beta_lactamase; 1.
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Amsterdam.'
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PROSITE; PS00146; BETA_LACTAMASE_A;

Hydrolase; Antibiotic resistance; S:

SIGNAL 1 21 POTENT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: Inhibited 16-fold better by the inhibitor clavulanic acid than by tazobactam. SIMILARITY: Belongs to the class-A beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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178; Conserv
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1 21 POTENTIAL.
22 286 BETA-LACTAMASE
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l (Rel. 40, Last annot
mase SHV-8 precursor
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BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
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DT 01-MAY-1991 (
DT 10-OCT-2003 (
DE Beta-lactamas
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RHSSP; P14557; 1SHV.

InterPro; IPR001466; Beta_lactamase_A.

InterPro; IPR001871; Beta_lactamase_A.

Pfam; PF00144; beta-lactamase; 1.

PFINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE A; 1.

PROSITE; PS00146; BETA_LACTAMASE A; 1.

PROSITE; PS00146; BETA_LACTAMASE SIGNAL.

RHYdrolase; Antibiotic resistance; Signal.

SIGNAL 1 21 POTENTIAL.

CHAIN 22 286 BETA-LACTAMASE SHV-8.

ACT_SITE 66 66 BY SIMILARITY.

PISULFID 73 119 BY SIMILARITY.

BINDING 230 232 SUBSTRATE (BY SIMILARITY).

SEQUENCE 286 AA; 31223 MW; F159990BC8BF5504 CRC64;
   Beta-lactamase
BLA OR SHV2.
Escherichia col
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SEQUENCE FROM N.A.

MEDLINE=97209066; PubMed=9056008;

Rasheed J.K., Jay C., Metchock B., Berkowitz F., Weigel L.,

Crellin J., Steward C., Hill B., Medeiros A.A., Tenover F.C.

"Evolution of extended-spectrum beta-lactam resistance (SHV strain of Escherichia coli during multiple episodes of bact antimicrob. Agents Chemother. 41:647-653(1997).

-i- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOS NOTABLY CEFOTAXIME AND CEFTAZIDIME.

-i- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substitut
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[1]
SEQUENCE FROM N.
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SIMILARITY: Belongs to the class-A
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bacteremia.
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SEQUENCE FROM N.A.
SPECIES=K.pneumoniae; STRAIN=KPLA-10;
MEDLINE=97291235; PubMed=9145849;
Nuesch-Inderbinen M., Kayser F.H., Hach
"Survey and molecular genetics of SHV k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=K.pneumoniae;
SPECIES=B.0264317; PubMed=2160941;
MEDLINE=90264317; PubMed=2160941;
Lee K.Y., Hopkins J.D., Syvanen M.;
"Direct involvement of IS26 in an ar
J. Bacteriol. 172:3229-3236(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=K.pneumoniae; STRAIN=KPR 14; Pl MEDLINE=91237320; PubMed=2033379; Podbielski A., Schoenling J., Melzer B "Molecular characterization of a new plactamase (SHV-2 variant) conferring hupon Klebsiella pneumoniae."; J. Gen. Microbiol. 137:569-578(1991).
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SEQUENCE FROM N.A.
SPECIES=K.pneumoniae; STRAIN=KPZU-3;
SPECIES=B.00740; PubMed=7486909;
MEDLINE=96100740; PubMed=7486909;
Nuesch-Inderbinen M., Hachler H., Kayser F.H.;
Nuesch-Inderbinen M., Hachler H., Kayser F.H.;
"New system based on site-directed mutagenesis for highled comparison of resistance levels conferred by SHV beta-1;
"The comparison of resistance levels conferred by SHV beta-1;
"The comparison of resistance levels conferred by SHV beta-1;
"The comparison of resistance levels conferred by SHV beta-1;
"The comparison of resistance levels conferred by SHV beta-1;
"The comparison of resistance levels conferred by SHV beta-1;
"The comparison of resistance levels conferred by SHV beta-1;
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SPECIES=K.ozaenae; STRA
MEDLINE=90370479; PubMe
Podbielski A., Melzer B
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Klebsiella pneumoniae (subsp. o
Salmonella typhimurium.
Plasmid pBWH77, Plasmid pZMP1,
Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Escherichia
NCBI TaxID=562, 573, 574, 602;
                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=S.typhimurium; PLASMID=pHT1;
SPECIES=S.typhimurium; PLASMID=pHT1;
SPECIES=S.typhimurium; PLASMID=pHT1;
MEDLINE=90351141; Pubmed=2201259;
Garbarg-Chenon A., Godard V., Labia
"Nuncleotide sequence of SHV-2 beta-1
"Nuncleotide sequence of SHV-2 heta-1
"Nuncleotide sequence of SHV-2 heta-1
SEQUENCE F
                                                      Garbarg-Chenon A., Godard V., "Nucleotide sequence of SHV-2 Antimicrob. Agents Chemother.
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PLASMID=pBP60-1;

PLASMID=p136192; PubMed=2285285;

MEDLINE=91136192; PubMed=2285285;

Huletsky A., Couture F., Levesque R.C.;

"Nucleotide sequence and phylogeny of SHV-2 beta-lactama antimicrob. Agents Chemother. 34:1725-1732(1990).
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"Nucleotide sequence of the gene
(blaSHV-2) of Klebsiella ozaenae.
Nucleic Acids Res. 18:4916-4916(1
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Podbielski A., Schoen
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Barthelemy M., Peduzzi J., Yaghlane H.B.
"Single amino acid substitution between
cefotaxime-hydrolyzing SHV-2 enzyme.";
FEBS Lett. 231:217-220(1988).
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E.coli; STRAIN=A2302; PLASE 1016385; PubMed=3129309;
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34:1444-1
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EMBL; X53433; CAA37524.1; -.

EMBL; X53817; CAA37813.1; -.

EMBL; X84314; CAA59058.1; -.

EMBL; X84314; CAA59058.1; -.

EMBL; M95179; AAA25526.1; -.

EMBL; X98102; CAA66730.1; -.

EMBL; AF148851; AAD37413.1; -.

PIR; A44998; A44998.

HSSP; P1457; 1SHV.

InterPro; IPR001466; Beta_lactamase.

InterPro; IPR001466; Beta_lactamase_A.

Pfam; PF00144; beta-lactamase; 1.

PRINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE A; 1.

Hydrolase; Antibiotic resistance; Plasmicular.
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"Automated thermal cycling is superior to traditinucleotide sequencing of blaSHV genes.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ datele-i- FUNCTION: This enzyme hydrolyzes cefotaxime,
broad spectrum cephalosporins.
-i- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a
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22 286
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73 119
230 232
31 31
36 AA; 31254 N
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PASMAERNQQIAGIGAALI
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.larity 67.9%;
Conservative 38
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                                                 STANDARD;
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BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
L -> Q (IN SHV-2A).
W; 738F4266651F551A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 936; DB 1;
Pred. No. 4.4e-67;
3; Mismatches 46
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me, ceftazidime
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Matches 178
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HSSP; P14557; ISHV.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
pfam; PF00144; beta-lactamase; 1.
pRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
Hydrolase; Antibiotic resistance; Signal.
SIGNAL 1 21 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HKY741;
STRAIN=HKY741;
STRAIN=HKY741;
Kurokawa H., Yagi T., Shibata N., Arakawa Y.;
Kurokawa H., Yagi T., Shibata N., Arakawa Y.;
"New SHV-derived extended-spectrum beta-lactamase gene.";
"New SHV-derived extended-spectrum beta-lactamase gene.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHAL
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ACT SITE
DISULFID
BINDING
SEQUENCE
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16-OCT-2001 (Rel. 40, Last annotation update)
Beta-lactamase SHV-24 precursor (EC 3.5.2.6).
BLA OR SHV24.
Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: SHV ENZYMES HYDROLYZE BRO NOTABLY CEFOTAXIME AND CEFTAZIDIME. CATALYTIC ACTIVITY: A beta-lactam + amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the class-A
                          242
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                                                                                                                                                                                                                                                                                    Similarity
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                                                  GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPK 121
                                                                                                                                                                                                                 PQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKV
                                                                                                                                                                                                                                  PETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKV
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PASMAERNQQIAGIGAALIEHW
                      QATMDERNRQIAEIGASLIKHW
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232
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BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
; 5EA9990BC8BOAAFF CRC64;
                           263
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                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
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RESULT 7
BLA3\_KLEPN
ID BLA3\_K
AC P30896
DT 01-JUL

STANDARD; 26,

BLA3\_KLEPN P30896; 01-JUL-1993

(Rel.

Created)

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RESULT
BLA5_KI
ID BI
AC P3
DT 01
DT 16
DE B6
GN BI
OS K1
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InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
Hydrolase; Antibiotic resistance; Plasmi SIGNAL 1 21
CHAIN 22 286
ACT_SITE 66 66
BY SIMILARI DISULFID 73 119
BINDING 230 232
SEQUENCE 286 AA; 31211 MW; 82715D986
              P37320;

01-OCT-1994 (Rel. 30, Cr

01-OCT-1994 (Rel. 30, La

16-OCT-2001 (Rel. 40, La

Beta-lactamase SHV-5 pre

BLA OR SHV5.

Klebsiella pneumoniae, a
                                                                                           KLEPN
BLA5_K
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HSSP; P14557; 1SHV.

InterPro; IPR001466; E

InterPro; IPR000871; E
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Nicolas M.H., Jarlier V., Honore N., Philippon A., Cole S.T.;
"Molecular characterization of the gene encoding SHV-3 beta-lactamase responsible for transferable cefotaxime resistance in clinical isolates of Klebsiella pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-lactamase
BLA OR SHV3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26,
10-OCT-2003 (Rel. 42,
Beta-lactamase SHV-3 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrob.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid.
SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        imicrob. Agents Chemother. 33:2096-2100(1989).
FUNCTION: This enzyme hydrolyzes cefotaxime, obroad spectrum cephalosporins.
CATALYTIC ACTIVITY: A beta-lactam + H(2)0 = a
                                                                                            KLEPN
                                                                                                                                                 263
                                                                                                                                                                                        203
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286 /
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(Rel. 30, Last seque)
(Rel. 40, Last annouse SHV-5 precursor
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        aeruginosa
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annotation update)
rsor (EC 3.5.2.6).
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BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
W; 82715D986508F50D CRC64;
                                                                                                                                                                                                                                                                                                                                                           Score 933; DB
Pred. No. 7.7e
97; Mismatches
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Plasmid;
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7.7e-67;
hes 47;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=K.pneumoniae;
MEDLINE=91207045; PubMed=2088203;
MEDLINE=91207045; PubMed=2088205;
MEDLINE=91207045; PubMed=2088205;
MEDLINE=91207045; PubMed=2088205;
MEDLINE=91207045; PubMed=2088205;
MEDLINE=91207045; PubMed=2088205;
MEDLINE=91207045; PubMed=2088205;
MEDLINE=9120705; PubMed=2088205; PubMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=P.aeruginosa;
Scoulica E., Aransay A., Tselentis
"Extended spectrum beta-lactamase (
clinical strain.";
Submitted (OCT-1998) to the EMBL/Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97291235; PubMed=9145849; Nuesch-Inderbinen M., Kayser F.H., "Survey and molecular genetics of Enterobacteriaceae in Switzerland:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=K.pneumoniae;
MEDLINE=97291235; Publ
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Enterobacteriaceae; Klebsiella.
NCBI_TaxID=573, 287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid.
SIMILARITY: Belongs to the class-A
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177; Conser
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  FROM
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ilarity 67.6%;
Conservative 39
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                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                     BETA-LACTAMASE SHV-5.
BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
W; 738F426CC51F5FBA CRC64;
                                                                                                                                                                                                                          Score 932;
Pred. No. 9.
9; Mismatche
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SHV-5
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9.2e-67;
hes 46
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SHV-11 and
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AANLLLATVGGPA 142
                                                     AANLLLTTIGGPK 121
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X MEDLINE=90146269; PubMed=2694955;

X Peduzzi J., Barthelemy M., Tiwari K., Mattioni D., Labia R.;

Y reftazidime of plasmid-mediated to hydrolytic activity against

Y reftazidime of plasmid-mediated SHV-type CAZ-5 beta-lactamase.";

X Antimicrob. Agents Chemother. 33:2160-2163(1989).

Y FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS

Y C -!- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS

Y C -!- CATALYTIC ACTIVITY: AND CEFTAZIDIME. SHV-4 CAUSES PARTICULARLY HIGH

Y C -!- SIMILARITY: Belongs to the class-A beta-lactamase family.

Y SIMILARITY: Belongs to the class-A beta-lactamase family.

R HSSP; P14557; 1SHV.

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Best Local S
Matches 177
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01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequentic Company (Rel. 40, Last anno Reta-lactamase SHV-4 (EC 3.5.2.
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STRAIN=210-2;
MEDLINE=90146269;
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Klebsiella pneumoniae.
Plasmid pUD21.
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il Similarity 67.6%;
177; Conservative 3:
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annotation update)
.5.2.6) (Ceftazidimase
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RESULT 10
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Matches 170
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PIR; A24469; A24469.
HSSP; P14557; 1SHV.
InterPro; IPR001466; Beta_lactam.
InterPro; IPR000871; Beta_lactam.
Pfam; PF00144; beta-lactamase; 1
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE.
Hydrolase; Antibiotic resistance
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13-AUG-1987 (Rel
01-OCT-1994 (Rel
Beta-lactamase p
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SEQUENCE
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-I- CATALYTIC ACTIVITY: A beta-lactam + H(2)0
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ACT SITE
DISULFID
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=LEN-1;
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-!- SIMILARITY: Belongs
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                                                                                                                                                                                                                                                                                Hydrolase;
SIGNAL
                                                                                                                                                                                                                        SEQUENCE
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Similarity 66.7%;
70; Conservative 38
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PASMAERNQQIAGIGAALIEHW
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LIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGR
                                                                                            GQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPK 121
                                                                                                                             PETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKV
                                   GLTAFLRQIGDNVTRLDRWETALNEALPGDARDTTTPASMAATLRKL
                                               ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLL
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1 (Rel. 30, Last anno
1 (Rel. 30, EC 3.
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Beta_lactamase_A.
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cesistance; S
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st annotation update)
(EC 3.5.2.6) (Penicillinase)
                                                                                WW.
                                                                                                                                                                           Score 905; DB 1; ]
Pred. No. 1.2e-64;
38; Mismatches 47;
                                                                                                                                                                                                                        BETA-LACTAMASE.
BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
5. C5C88E34E6BCDAEB CRC64;
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Signal.
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                                    TAQHLSARSQQQ 202
                                                                                    GNLLLATVGGPA 142
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PSRIVVIYTTGS 241
                                                           TGELLTLASRQQ 181
                                                                                                                                 LCGAVLARVDA 82
                                                                                                                                                        LCGAVLSRIDA 61
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RESULT 11
BLA6_KLEPN
ID BLA6_K
AC P96348
AC Entero
OX Klebsi
OC Bacter
OC NCBI_T
RN MEDLIN
RX MEDLIN
RY CC -i- FU
CC -i- FU
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Matches 168
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SEQUENCE FROM N.A.
STRAIN=SLK-47;
MEDLINE=97372563; PubMed=9228783;
Arlet G., Rouveau M., Philippon A.;
"Substitution of alanine for aspartate at poextended-spectrum beta-lactamase.";
FEMS Microbiol. Lett. 152:163-167(1997).
-!- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SP.
NOTABLY CEFCTAXIME AND CEFTAZIDIME.
-!- CATALYTIC ACTIVITY: A beta-lactam + H(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y11069; CAA71948.1; -.
HSSP; P14557; 1SHV.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; beta_lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
Hydrolase; Antibiotic resistance; Signal.
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NON_TER
SEQUENCE
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ACT SITE
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae.
Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Klebsiella
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P96348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid.
SIMILARITY: Belongs to the class-A beta-lactamase family.
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ELTAFLHNMGDHVTRLDRWEPBLNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQQ
                                                           POPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDA
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larity 67.7%;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
ase SHV-6 precursor (EC 3.5.2.6) (
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                                                                                                                                                                                                                                                       Score
Pred.
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BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY S.
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                                                                                                                                                                                                                                ore 879; DB 1;
red. No. 1.3e-62;
Mismatches 45;
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RESULT 12
BLA1_ENTCL
ID BLA1_E
AC P18251
DT 01-NOV
DT 01-OCT
DE Beta-1
OS Enterc
OG Plasmi
OC Enterc
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01-NOV-1990 (Rel. 16, L
01-OCT-1994 (Rel. 30, L
Beta-lactamase Ohio-1 p:
Enterobacter cloacae.
Plasmid pDS075
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PIR; A44958; A44958.
HSSP; P14557; 1SHV.
InterPro; IPR001466; Beta lactam
InterPro; IPR000871; Beta lactam
Pfam; PF00144; beta-lactamase; 1
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ACT SITE
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BINDING
SEQUENCE
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Hydrolase;
SIGNAL
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P18251;
01-NOV-1990
01-NOV-1990
01-OCT-1994
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PRINTS;
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SEQUENCE FROM N.A.

MEDLINE=91024125; PubMed=2121093;

Shlaes D.M., Currie-Mccumber C., Hull A., Behlau I., For the Ship of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Enterobacter.
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SIMILARITY: Belongs
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169; Conservative
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; PS00146; BETA LACTAMASE A; 1.
se; Antibiotic resistance; Signal;
                                                                                                                 GLTAFLRQIGDNVTRLDRWETELNEALPGDARDT
                                 ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKL
                                                                                                                                                                                                                                                                                          PETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFF
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Beta_lactamase_A.
lactamase; 1.
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precursor (EC 3.5.2.6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                      39;
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                                                                                                                                                                                                                                                                                                                                                            Score 874; DB 1; Pred. No. 3.6e-62; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JBSTRATE (BY SIMILARITY)
9FE16709361AF9C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          class-A
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LTSQRLSARSQRQ
                                                                                                                    AANLLLPAVGGPA 142
                                                                                                                                                                             AANLLLTTIGGPK 121
                                                    LTGELLTLASRQQ 181
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  202
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RESULT 13
BLAC PROMI
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Best Local
Matches 13
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PIR; A41381; A41381.

HSSP; P00810; ITEM.

InterPro; IPR001466; Beta_lactamase.

InterPro; IPR000871; Beta_lactamase_A.

Pfam; PF00144; beta-lactamase; 1.

PRINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE_A; 1.

Hydrolase; Antibiotic resistance; Signal SIGNAL

SIGNAL

28

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993
01-JUL-1993
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino act...

-!- SIMILARITY: Belongs to the continuous action.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sakurai Y., Tsukamoto K., Sawai T.;
"Nucleotide sequence and characterization of
carbenicillin-hydrolyzing penicillinase gene
mirabilis.";
J. Bacteriol. 173:7038-7041(1991).
-!- FUNCTION: Hydrolyzes carbenicillin.
-!- CATALYTIC ACTIVITY: A beta-lactam + H(2)(
                                                                                                                                                                                                                                        CHAIN
ACT SITE
BINDING
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92041595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=GN79;
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                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid. SIMILARITY: Belongs to the class-A beta-lactamase family.
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                                                                                              LVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRIDAGQE
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(Rel. 26, Last
(Rel. 42, Last
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29
72
237
237
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                                                                                                                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                                                                                  BETA_LACTAMASE_..,
otic resistance; Signal.
28 POTENTIAL.
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72 B
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126 MW;
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| PVTEKHVGKKGMSLAELCQATLSTSDNSAANFILQAIGGPKAL
                                                                                                                                                             48;
                                                                                                                                                    Score 672; из
Pred. No. 3.9e
48; Mismatches
                                                                                                                                                                                                                                                           BETA-LACTAMASE.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY)
BY SIMILARITY.
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(Carbenicillinase).
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                                                                                -HKSNERFPLSSTFKTLACANVLQRVDLGKE
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3.9e-46;
78;
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Matches 119
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BLA1 AE
Q44056;
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Sanschagrin F., Bejaoui ...,
Sanschagrin F., Bejaoui ...,
Sanschagrin F., Bejaoui ...,
Sanschagrin F., Bejaoui ...,
"Structure of CARB-4 and AER-1 carbeniciii...
"Structure of CARB-4 and AER-1 carbeniciii...

"action of CARB-4 and AER-1 carbeniciii...
"action of CARB-4 and AER-1 carbeniciii...
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         CHAIN
ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS
Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=VL7711; TRANSPOSON=Omega7711; MEDLINE=98353319; PubMed=9687391; Sanschagrin F., Bejaoui N., Levesque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
Aeromonadaceae; Aeromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM I
STRAIN=VL7711;
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HSSP; P14557; 1SHV.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00144; beta-lactamase; PRINTS; PR00118; BLACTAMASEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid. SIMILARITY: Belongs to the class-A beta-lactamase family.
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                                                                                                              47
                                                                                                                                                                                                                                           ch 42.6%;
il Similarity 47.0%;
119; Conservative 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO0118; BLACTAMASEA.

3; PS00146; BETA LACTAMASE A; 1.

1se; Antibiotic resistance; Signal POTENTIAL.
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RRIHYSQNDLVEYSPVTEKHLT-DGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAF 126
                                                                                                           VOSEESALHARVGMTVFDSNTGTTW-NYRGDERFPLNSTHKTFSCAAI
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R-1 carbenicillin-hydrolyzing
                                                                                                                                                                                                                                              Score 573; DB 1;
Pred. No. 2.8e-38;
5; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
SUBSTRATE (BY SIMI)
66AD56ED45D02A41
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BY SIMILARITY.
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Best Loc
Matches
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NCBI TaxID=287;
[1]
SEQUENCE FROM N.A.
STRAIN=Cilote; TRANSPOSON=Tn1408;
MEDLINE=91323732; PubMed=1650733;
Lachapelle J., Dufresne J., Levesque R.C.;
"Characterization of the blaCARB-3 gene encoding the carbenicillinase-3 beta-lactamase of Pseudomonas aerugii Gene 102:7-12(1991).
                                                                                                                                                           EMBL; S46063; AAB19430.2; ALT_INIT.
PIR; JQ1136; JQ1136.
HSSP; P14557; 1SHV.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
Hydrolase; Antibiotic resistance; Signal
                                                                                            ACT SITE
DISULFID
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSEAE
BLC3 PSEAE
P37322;
01-OCT-1994
01-OCT-1994
16-OCT-2001
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a coptween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                              CHAIN
ACT_SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria;
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                                               Local Sin
hes 116;
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VXAIEVSLSARIGVSVLDTQNGEYWD-YNGNQRFPLTSTFKTIACAKLLYDAEQGKVNPN
               VKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRIDAGQEQLG
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                                               42;
                                                                                       POTENTIAL.

BETA-LACTAMASE CARB-3.

BY SIMILARITY.

BY SIMILARITY.

SUBSTRATE (BY SIMILARITY).

SUBSTRATE (BY SIMILARITY).
                                            Score 539.5; DB 1;
Pred. No. 1.2e-35;
2; Mismatches 93;
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Usage by and for commercial
ttp://www.isb-sib.ch/announce/
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Search completed: June 18, 2004, 19:08:28 Job time : 18 secs

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						RESULT 1 S47061
	ALIGNMENTS					
beta-lactamase	JC4117		309	34.8	467.5	45
beta-lactamase			294	35.1	471.5	44
beta-lactamase	S23929	N	263	35.5	477	43
penicillinase			306	35.9	482.5	42
beta-lactamase			314	35.9	483	41
beta-lactamase	: G69674		306	35.9	483.5	40
beta-lactamase	2 A61156		305	36.4	489.5	. 65
beta-lactamase			305	36.4	489.5	О
beta-lactamase			305	36.4	489.5	37
beta-lactamase	: JP0074		291	36.5	491	36
beta-lactamase	B45822		306	36.8	494.5	ω G
beta-lactamase	S16553		294	36.9	496.5	34
beta-lactamase			302	37.6	505.5	, ω ω
beta-lactamase	S04649		293	38.1	512.5	32
beta-lactamase			263	38. <sub>1</sub>	512.5	i Gi
beta-lactamase			291	38,2	513.5	30

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beta-lactamase (EC 3.5.2.6) - phage phi-X:
C;Species: phage phi-X174
C;Date: 13-Jan-1995 #sequence_revision 13:
C;Accession: S47061
R;Henrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July :
A;Description: A variant of phiX174 gene I
A;Reference number: S47060
A;Accession: S47061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <HEN>
A;Cross-references: EMBL: Z35638; NID: 95208
C;Superfamily: beta-lactamase I
C;Keywords: hydrolase
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Best Local Similarity 98.9%;
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                                                                                                                                        KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
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                                                                                                                                                                                                                                                      HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMST
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                                                                               QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPL
                                                                                                                          KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRI
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SQATMDERNRQIABIGASLIKHW
                           SQATMDERNRQIAEIGASLIKHW
                                                             QLIDWMEADKVAGPLLRSALPAGWF
                                                                                                                                                                                                                                                                                                                     Score 1330; D
Pred. No. 3.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     NID:g520996;
                             263
286
                                                            IADKSGAGERGSRGI LAALGPI
                                                                                                                                                                                                                                                                                                                     DB 2;
.5e-103;
.es 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                    1; PID:g520998
                                                           OGKPSKIVVIYTTG 263
                                                                                                                                                                                                                                                                                    FKVLLCGAVLSRID 60
                                                                                                                                                                                        NTAANLLLTTIGGP 143
                                                                                                                                                                                                                 NTAANLLLTTIGGP 120
                                                                               )GKPSRIVVIYTTG 240
                                                                                                                                                                                                                                                       KVLLCGAVLSRID 83
                                                                                                                                                                                                                                                                                                                                                       286;
                                                                                                                      LLTGELLTLASRO 203
                                                                                                                                                                                                                                                                                                                     0; Gaps
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RESULT 2
T51301
beta-lactamase (EC 3.5.2.6) - fix
C; Species: Schizosaccharomyces po
C; Date: 18-Aug-2000 #sequence\_re
C; Accession: T51301
R; WACH, A.; BRACHAT, A.; ALBERTI:
Yeast 13, 1065-1075, 1997
A; Title: Heterologous HIS3 marke:

s pombe revision fission

18-Aug-2000

#text\_change 02-Sep-2000

yeast

(Schizosaccharomy

rces pombe)

ALBERTISEGUI,

c.;

REBISCHUNG,

C.;

PHILIPPSEN, P.

marker

and

GFP

reporter

modules

for PCR-targeting in Saccharo

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Deta-lactamase (EC 3.5.2.6) precursor - synthetic C; Species: synthetic C; Species: synthetic C; Date: 25-Dec-1994 #sequence_revision 22-Aug-1996 #text_chan C; Accession: S41975 R; Kaestner, K.H.; Montoliu, L.; Kern, H.; Thulke, M.; Schutz, Gene 148, 67-70, 1994 A; Title: Universal beta-galactosidase cloning vectors for pro A; Reference number: A57991; MUID:95011660; PMID:7926839 A; Accession: S41975 A; Status: not compared with conceptual translation A; Molecule type: DNA A; Residues: 1-286 < KAE> A; Cross-references: EMBL:X76682; NID:g453622; PIDN:CAA54104.1 A; Note: submitted to the EMBL Data Library, December 1993 C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: Z0958
A;Accession: T51301
A;Status: preliminary; tr
A;Molecule type: DNA
A;Residues: 1-286 <WAC>
A;Cross-references: EMBL:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: bla
C;Superfamily: beta-lactamase
C;Keywords: hydrolase
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Best Local S
Matches 260
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Best Local S
Matches 260
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hes 260;
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Similarity 98.9%;
60; Conservative
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                                                                                                                                                     AGQEQLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                               HPETLVKVKDAEDQLGARVGYIBLDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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                                                                 KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTT
                  QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                  KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ
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1; Mismatches
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Pred. No. 3.5e-103;
1; Mismatches 2;
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1es 2;
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A; Molecule type: protein
A; Residues: 24-36, 'K', 38-286 < AMB>
A; Residues: 24-36, 'K', 38-286 < AMB>
A; Experimental source: plasmid R6K
R; Kornacki, J.A.; Burlage, R.S.; Figurski, D.
J. Bacteriol. 172, 3040-3050, 1990
A; Title: The kil-kor regulon of broad-host-ra
A; Reference number: A35387; MUID:90264294; PM
A; Accession: A35387
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Proc. Natl. Acad. Sci. U.S.A. 75, 3737-3741, 1978 A;Title: Nucleotide sequence of the ampicillin resistance gene A;Reference number: A93821; MUID:79012484; PMID:358200 A;Accession: A93821
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A; Residues: 1-286 <SUT>
A; Cross-references: GB:V00613; GB:J01832; NID:g43710; FA; Cross-references: GB:V00613; GB:J01832; NID:g43710; FA; Cross-references: GB:V00613; GB:J01832; NID:g43710; FA; Cross-reference: GB:V00613; GB:J01832; NID:g43710; FA; Cross-reference: A; Title: Partial amino acid sequence of penicillinase ca; Title: Partial amino acid sequence of penicillinase ca; Reference number: A93820; MUID:79012483; PMID:358199 A; Reference: A93820; MUID:79012483; PMID:358199 A; Molecula: Ap3820; MUID:79012483; PMID:35819 Ap3820; MUID:79012483; PMID:79012483; P
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A; Residues: 182-286 < KOR>
A; Cross-references: GB: M32794; NID: g152521;
A; Experimental source: PK2
A; Experimental source: PK2
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R;Sutcliffe, J.G.

Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979

A;Title: Complete nucleotide sequence of the Escherichia A;Reference number: A90923; MUID:80002802; PMID:383387

A;Contents: annotation
C;Comment: Like most penicillinases from gram-negative ba
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A;Residues: 1-101,'K',103-161,'H',163-286 <GC
A;Cross-references: EMBL:X57972; NID:g41816;
A;Experimental source: ISI-like blaT-6 DNA
                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase; membrane
C;Keywords: signal sequence #status predicted <SIG>
F;1-23/Domain: signal sequence #status experimental .
F;24-286/Product: beta-lactamase #status experimental .
F;68/Active site: Ser #status predicted
F;75-121/Disulfide bonds: #status predicted
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Best Local Similarity
Matches 258; Conser
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                                                                                      HPETLVKVKDAEDQLGARVGYIELDLNSGEILESERSEERFPMMSTFKVLLCGAVLSRID 60
AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDN
                                                                                                                                                                                                                                         98.5%;
ilarity 98.1%;
Conservative
                                                                                                                                                                                                                                         Score 1325; DB 1;
Pred. No. 9.1e-103;
2; Mismatches 3;
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PMID:1665171
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                                                                                                                                                                                                                                                                                                                                  286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid pBR322.
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extended spectrum beta-lactamase CAZ-7 - Klebsiella pr
C;Species: Klebsiella pneumoniae
C;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #te
C;Accession: S60312
R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sir
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-1, CAZ-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
I40905
beta-lactamase (EC 3.5.2.6) - synthetic
C; Species: synthetic
A; Note: cloning vector pCG1408 engineered and
C; Date: 15-Aug-1996 #sequence_revision 16-Aug-
C; Accession: I40905
R; Taylor, J.; Stearman, R.S.; Uratani, B.B.
Plasmid 29, 241-244, 1993
A; Title: Development of a native plasmid as a A; Reference number: 140904; MUID:93361581; PMI
A; Accession: I40905
A; Status: preliminary; translated from GB/EMBL
A; Residues: 1-286 < RES>
A; Cross-references: EMBL:U21228; NID:9885956; C; Keywords: hydrolase
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S60312
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Best Local S
Matches 258
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nes 258; Conserv
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ilarity 98.1%;
Conservative
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Pred. No. 9.1e-103;
2; Mismatches 3;
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                                                                                      2-6, and CAZ-
PMID:1416873
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RESULT 7

$30113
beta-lactamase (EC 3.5.2.6) TEM-3 - Klebsiell
C;Species: Klebsiella pneumoniae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep
C;Accession: $30113
R;Mabilat, C.; Lourencao-Vital, J.; Goussard,
Mol. Gen. Genet. 235, 113-121, 1992
A;Title: A new example of physical linkage be
A;Reference number: $30112; MUID:93062798; PM
A;Accession: $30113
A;Status: translation not shown
A;Residues: 1-286 <MAB>
A;Residues: 1-286 <MAB>
                                                                                                                                                                                                                                                                                                                                                              A;Gene: bla(TEM-3)
A;Genome: plasmid
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: C; Genetics:
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Best Local Similarity
Matches 255; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
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Best Loc
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;Superfamily: beta-lactamase I
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Local Similarity 97.0%;
les 255; Conservative
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                                                                        QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPL
                                                                                                                                   KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRI
                                                                                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTI
                         SQATMDERNRQIAEIGASLIKHW
                                                                                                                                                                                                                                         HPETLVKVKDAEDKLGARVGYIELDLNSGKILESFRPEERFPMMST
 SQATMDERNRQIAEIGASLIKHW
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ilarity 97.0%;
Conservative
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                                                                                                                    DRWEPELNEAL
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                                                                                                                                                                                                                                                                                                     Score 1311; DB 2;
Pred. No. 1.3e-101;
k; Mismatches 4;
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Pred. No. 1.1e-101;
; Mismatches 4;
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286
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PMID:1331747
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                                                                                                                                                                                                                                     FKVLLCGAVLSRVD 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PID:g43798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asmid pCFF04
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                                                                        )GKPSRIVVIYTTG 240
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                                                       GKPSRIVVIYTTG 263
                                                                                                                                                                                                                                                          |KVLLCGAVLSRID 60
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                                                                                                                                    LTGELLTLASRQ 180
                                                                                                               RELLTLASRO 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                 Gaps
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A; Residues: 1-32 <TOL>
A; Cross-references: GB:NC; Genetics:
A; Gene: TEM-bla
C; Superfamily: beta-lact
C; Keywords: antibiotic r
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A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactama: A;Reference number: S60310; MUID:93037315; PMID:1416873
A;Accession: S60310
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-286 < CHA>
A;Residues: 1-286 < CHA>
A;Cross-references: EMBL:X65252; NID:g296951; PIDN:CAA46344.1; PID:g29C;Superfamily: beta-lactamase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                extended spectrum beta-lactamase CAZ-2 C;Species: Klebsiella pneumoniae C;Date: 12-Apr-1996 #sequence_revision C;Accession: S60310 R;Chanal, C.; Poupart, M.C.; Sirot, D.;
                                                                                                                                     A;Cross-references: EMBL:X65253; NID:g296953; PIDN:CAA4639
R;Tolmasky, M.E.
R;Tolmasky, M.E.
Plasmid 24, 218-226, 1990
A;Title: Sequencing and expression of aadA, bla, and tnpR
A;Reference number: A37392; MUID:91172904; PMID:1963948
A;Recession: F37392
A;Molecule type: DNA
A;Residues: 1-32 <TOL>
                                                                                                                                                                                                                                                                                                                                             beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Species: Klebsiella pneumoniae C;Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text_C;Accession: S60311; F37392; FQ0498
R;Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A;Title: Nucleotide sequences of CAz-2, CAz-6, and CAZ-7, Reference number: S60310; MUID: 93037315; PMID: 1416873
A;Accession: S60311
                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translation not A;Molecule type: DNA
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1-286 <CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ
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                                                                          beta-lactamase
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                                                                                                                            GB:M55547; NID:g155010;
                                                       resistance;
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96.6%;
96.9%;
96.2%;
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Pred. No. 4.2e-101;
4; Mismatches 5;
                                                                                                                                                                                                                                                                          NID:g296953; PIDN:CAA46345.1;
 Score
Pred.
                                                       hydrolase
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 1303;
No. 6.
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  DB 2;
.1e-101;
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                     286;
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A; Title: Complete nucleotide sea; Reference number: JQ1538; MU: A; Accession: JQ1546
A; Status: translation not shown A; Molecule type: DNA
A; Residues: 1-286 < CAN>
C; Genetics:
RESULT 11
S00464
beta-lactamase
N;Alternate name
C;Species: Esche
C;Date: 31-Dec-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bla protein - Salmonella typhimurium pl
N;Alternate names: beta lactamase homol
C;Species: Salmonella typhimurium
C;Date: 30-Sep-1993 #sequence_revision
C;Accession: JQ1546
R;Cannon, P.M.; Strike, P.
Plasmid 27, 220-230, 1992
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JQ1546
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 mase (EC 3.5.2.6) class
e names: beta-lactamase
Escherichia coli
-Dec-1988 #sequence_revi
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                                                                                                                                                        QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGYSGIIAALGPDGKPSRIVVIYTTG 263
                                                                                                        SQATMDERNRQIAEIGASLIKHW
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Pred. No. 1.3e-100;
2; Mismatches 7;
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                          A - Escherichia
PIT-2; beta-lact
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                             beta-lactamase
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; PMID:1325061
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revision

31-Dec-1988

\_change 18-Jun-1993

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beta-lactamase (EC 3.5.2.6) 2A precursor - Klebsiella N;Alternate names: beta-lactamase SHV2A C;Species: Klebsiella pneumoniae C;Accession: S16146; A35395; S18767 R;Podbielski, A.; Schoenling, J.; Melzer, B.; Warnatz, J. Gen. Microbiol. 137, 569-578, 1991 A;Title: Molecular characterization of a new plasmid-e A;Reference number: S16146; MUID:91237320; PMID:203337 A;Accession: A35395; MUID:91237320; PMID:CAA3 A;Accession: A35395 MUID:90264317; PMID:216094 A;Accession: A35395 MUID:902
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R;Barthelemy, M.; Peduzzi, J.; Labia, R.
Biochem. J. 251, 73-79, 1988
A;Title: Complete amino acid sequence of p453
A;Reference number: S00464; MUID:88268817; PM
A;Accession: S00464
A;Molecule type: protein
A;Residues: 1-265 <BAR>
C;Genetics:
A;Genome: plasmid
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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nilarity 68.3%;
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Pred. No. 6.2e
98; Mismatches
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Pred. No. 1e-70;
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No. 6.2e-71;
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; PMID:2160941
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1; PMID:3260490
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R;Garbarg-Chenon, A.; Godard, V.; Labia, R.; Nicolas, J.
Antimicrob. Agents Chemother. 34, 1444-1446, 1990
A;Title: Nucleotide sequence of SHV-2 beta-lactamase ger
A;Reference number: A60679; MUID:90351141; PMID:2201259
A;Accession: A60679
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <GAR>
A;Cross-references: GB:L47119; NID:g972890; PIDN:AAA7501
C;Genetics:
A;Genome: plasmid
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
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beta-lactamase
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8; Mismatches
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PMID:2201259
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LLTSQRLSARSQRQ 202
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beta-lactamase (EC 3.5.2.6) C;Species: Escherichia coli C;Date: 01-Dec-1989 #sequen

#sequence

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#text

\_change 18-Jun-1993

SHV-2

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Escherichia

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RESULT S02434

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C;Accession: S02434
R;Barthelemy, M.; Peduzzi, J.; Yaghlane, H.B.; Labia, R.
FEBS Lett. 231, 217-220, 1988
A;Title: Single amino acid substitution between SHV-1 beta-lactamase A;Reference number: S02434; MUID:88196385; PMID:3129309
A;Accession: S02434
A;Molecule type: protein
A;Residues: 1-265 <BAR>
C;Superfamily: beta-lactamase I
C;Keywords: antibiotic resistance; hydrolase
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A; Residues: 1-286 <HUL>
A; Residues: 1-286 <HUL>
A; Cross-references: GB: M95179; NID: g150488; PIDN: AAA25526.1; PID: g150489
R; Podbielski, A.; Melzer, B.
Nucleic Acids Res. 18, 4916, 1990
Nucleic Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase A; Reference number: S12703; MUID: 90370479; PMID: 2395654
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A; Cross-references: EMB
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C;Superfamily: beta-lactamase
C;Keywords: antibiotic resista
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69.6%; Score 936; DB 2; Length 265; ilarity 67.9%; Pred. No. 2e-70; Conservative 38; Mismatches 46; Indels
                                                                                                                                                                                                                                        EMBL:X53433; NID:g43789; PIDN:CAA37524.1; PID:g43790
                                                                                                                                                          resistance; hydrolase
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                                                                             69.6%; Score 936; DB 1; 67.9%; Pred. No. 2.2e-70; ive 38; Mismatches 46
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Search completed: June 18, Job time : 21 secs 2004, 19:09:01

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Perfect score:
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Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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length: 2000000000
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1515.275 Million cell updates/sec
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1330	1330	1330	1330	1330	1330	1330	1330	1330	1330	1330	1330	1330	1330	1330	Score
98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	98.9	Query Match Length
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Sequence 16, Appl	Sequence 9, Appli	Sequence 2, Appli	16,	9	2, 4		21,	14	7,		Sequence 21, Appl	14,	Sequence 7, Appli	Sequence 2, Appli	Description

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Sequence 73015, A	Sequence 175764,	28	e u	2		65	e 10	10,	e 1,	e L	760, Ap	7	o,	3, Appl	equence 2	e 3, Appl	equence 3	ce 8, Āppl	9, Appli	Ф Ф	8, Appli	N	4, Appl	e 5, Āppl	7, Appli	ce 2	6, Appli	equence 292, Āp	Sequence 9, Appli

## ALIGNMENTS

US-10-668-778-2

Sequence 2, Application US/10668778 Publication No. US20040038317A1 GENERAL INFORMATION:

```
APPLICANT: Her. Jeng-Horng
APPLICANT: Her. Jeng-Horng
APPLICANT: KaloBios, Inc.
ITITLE OF INVENTION: Interaction-Activated Proteins
FILE REFERENCE: 021167-000700US
CURRENT APPLICATION NUMBER: US/10/668,778
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US/09/526,106
PRIOR FILING DATE: 1090-03-15
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR APPLICATION NUMBER: US 60/124,339
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SED ID NOS: 26
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SED ID NOS: 26
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 2000-01-13
NUMBER OF SED ID NOS: 26
PRIOR FILING DATE: 2000-01-13
NUMBER OF SED ID NOS: 26
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 60/175,968
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-03-1
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; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; General INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; TILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 1020-02
; PRIOR APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 1999-02-08
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
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US-09-919-901-7
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RESULT 3
US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
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OTHER INFORMATION: :
-09-919-901-7
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Sequence 21, Application US/09919901
; publication No. US20030082518A1
; GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CEI
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C V
FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 286
TYPE: PRT
CORGANISM: Artificial Sequence
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CEL

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C V

FILE REFERENCE: 0125-000F3A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
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; OTHER INFORMATION:
US-09-919-901-14
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US-09-919-901-21
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Best Local Similarity
Matches 260; Conserv
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TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION:
                 FEATURE:
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98.9%;
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Pred. No. 7.3e-129;
1; Mismatches 2;
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US-09-919-901-21

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APPLICANT: LADWARD H.

APPLICANT: LADWARD H.

APPLICANT: COHEN, EDWARD H.

APPLICANT: NASTRI, HORACIO G.

APPLICANT: NOKEY, KRISTIN L.

APPLICANT: HOET, RENE

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC TITLE OF INVENTION: DIVERSE THAT COLLECTIVELY DISPLAY THE MEMBERS OF A TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS FILE REFERENCE: DYAX/002

CURRENT APPLICATION NUMBER: US/09/837,306

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/198,069

PRIOR FILING DATE: 2000-04-17

NUMBER OF SEQ ID NOS: 428

SOFTWARE: PatentIn Ver. 2.1

ENGTH: 286
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; OTHER INFORMATION: Description of Unknown Organism:
US-09-837-306-354
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Best Local Similarity
Matches 260; Conserv
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ORGANISM: Unknown
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QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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Conservative
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nilarity 98.9%;
Conservative
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Pred. No. 7.3e-129;
1; Mismatches 2;
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Sequence 7, Application US/10191966

Publication No. US20030175692A1

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CEITITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C V.

FILE REFERENCE: 0125-005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

COETWARE DESCRIPTION OF THE HEPATITIS C V.
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US-10-191-966-14
; Sequence 14, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
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US-10-191-966-7
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Best Local S
Matches 260
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                BASED ASSESSMENT
US PROTEASE
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Sequence 21, Application US/10191966
; Sequence 21, Application No. US20030175692A1
; GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FITTLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
CURRENT APPLICATION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NO.21
; ENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: :
US-10-191-966-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,6:
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; SEQ ID NO 14
; LENGTH: 286
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US-10-191-966-21
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Best Local Similarity
                                                                   Query Match
Best Local Similarity
Matches 260; Conserv
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ORGANISM: Artificial
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                  HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID
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Pred. No. 7.3e-129;
                                                                    Score 1330; DB 14;
Pred. No. 7.3e-129;
1; Mismatches 2;
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CURRENT APPLICATION NUMBER: US/10/045,67
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 523
LENGTH: 286
TYDE: PRT
                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: protein sequence US-10-045-674-523
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US-10-045-674-523
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APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
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Best Local Similarity
Matches 260; Conserv
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APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF ITILE OF INVENTION: DISPLAYED, POLYPEPTIDES OR PROTEINS ITILE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
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SQATMDERNRQIAEIGASLIKHW
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                                              QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSR
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5. US20030232333A1
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98.9%;
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Pred. No. 7.3e-129;
1; Mismatches 2;
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AND THE NOVEL
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RESULT 11

US-09-919-901-9

; Sequence 9, Application US/09919901

; Publication No. US20030082518A1

; GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

; APPLICANT: Patick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CEL:

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C V.

; FILE REFERENCE: 0125-0005A

; CURRENT APPLICATION NUMBER: US/09/919,901

; CURRENT APPLICATION NUMBER: 09/263,933

; PRIOR APPLICATION NUMBER: 09/263,933

; PRIOR APPLICATION NUMBER: 09/129,611

; PRIOR APPLICATION NUMBER: 09/129,611

; PRIOR FILING DATE: 1998-08-05

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0
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Publication No. US20030082518A1

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
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US-09-919-901-2
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Best Local Similarity 98.9
Matches 260; Conservative
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ENGTH: 2307
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Pred. No. 1.5e-127;
1; Mismatches 2;
                                                                                                                                                                                                 CELL-BASED ASSES
C VIRUS PROTEASE
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
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; OTHER INFORMATION:
US-09-919-901-16
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US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 260; Conserv
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS
FILE REFERENCE: 0125-0005A
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LENGTH: 2307
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TYPE: PRT
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OTHER INFORMATION:
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ORGANISM: Artificial Sequence
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                                                     AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDN
                                                                                            HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60
                                                                                                               HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTF
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KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
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                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVREL
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                                                                                                                                                            98.9%; Score 1330; DB 10; 98.9%; Pred. No. 1.5e-127; cive 1; Mismatches 2;
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Pred. No. 1.5e-127;
l; Mismatches 2;
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US PROTEASE
                                                 TAANLLLTTIGGP 120
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RESULT 13
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                                                                                                                                    RESULT 14
US-10-191-966-9
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Sequence 9, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE
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LENGTH: 2307
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APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ.ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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98.9%;
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RESULT 15

US-10-191-966-16
; Sequence 16, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CEL
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C V
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
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Query Match
Best Local Sim
Matches 260;
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Best Local Similarity
Matches 260; Conserv
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                                                                                                                TYPE: PRT ORGANISM: Artificial
                                                                                FEATURE:
OTHER INFORMATION:
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; Score 1330; D
; Pred. No. 1.5e
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Pred. No. 1.5e-127;
1; Mismatches 2;
                 1.5e-127;
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Search completed: June 18, 2004, 19:15:27 Job time : 51 secs

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1 HPE     24 HPE	atch cal Simi 260;	REFERENCE/DOCKET NUMBER: P-32 TELECOMMUNICATION INFORMATION: TELEPHONE: (313) 689-3554 TELEFAX: (313) 689-4071 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 286 amino acids TYPE: AMINO ACID TOPOLOGY: linear MOLECULE TYPE: protein -07-721-775A-2	COMPUTER: LBM PC COM OPERATING SYSTEM: PC SOFTWARE: PATENTIN RC CURRENT APPLICATION DAT APPLICATION NUMBER: FILING DATE: 1991062 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMAT NAME: KOhn, Kenneth REGISTRATION NUMBER:	CITY: Troy STATE: Mich COUNTRY: U. ZIP: 48099 COMPUTER READA MEDIUM TYPE:		1-775A-2 ce 2, Appli No. 518066 AL INFORMAT	441	1310.5 1310.5 1300.5 1308 1308 1308 942 449	1320 1318 1318 1318 1318 1317 1317	1325
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EDQLG	98.9 98.9 ive	TICS: acid	Compati PC-DOS In Relea DATA: US/0 10627 435 eth I. ER: 30.	FORM:	METH METH MUTH MUTH MUTH 2 2 2 2 SS: UG, Et	J. Ch	192	262 262 286 286 244 244 247	22222222222222222222222222222222222222	286 286
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IELDLNSGEILESFRSE 	Score 1330; DB 1; Length Pred. No. 7.1e-139; 1; Mismatches 2; Indel	P-321WSU DN:	ble /MS-DOS se #1.0, Version #1.25 7/721,775A		RAYMOND F. AND CELL LINE FOR TESTI NICITY OF A CHEMICAL	ation US/07721775A ON: tes, J. Christopher		US-09-626-581D-3 US-09-415-765B-3 US-09-626-580C-3 US-08-346-333-16 PCT-US91-07506-16 US-09-489-039A-11425 US-09-489-039A-9803 US-09-489-039A-11509		4 - 4
ERFPMMSTFKVLLCGAVLSRID 60	h 286; ls 0; Gaps 0;				NG Milton		9460,	Appl Appl Appl Appl , App , App 425, 03, A	11407, 6, App 6, App 6, App 6, App 8, App 8, App	4, Appl 4, Appl

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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: pr
US-08-339-658-2

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PRIOR APPLICATION: 435

PRIOR APPLICATION NUMBER: US 07/990,295

FILING DATE: 09-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: KOHN, Kenneth I.
REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: P-321WSU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
TELEPAX: (313) 689-4071

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 5525482
GENERAL INFORMATION:
                                                                                                                                   Query Match 98.9%;
Best Local Similarity 98.9%;
Matches 260; Conservative
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APPLICANT: Hines, Ronald N.
APPLICANT: No. 5525482ak, Raymond F.
APPLICANT: No. 5525482ak, Raymond F.
TITLE OF INVENTION: METHOD AND CELL LINE FOR TITLE OF INVENTION: MUTAGENICITY OF A CHEMICA NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/339,658 FILING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: M
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CITY: T
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  AGOEOLGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                       Score 1330; DB 1; Pred. No. 7.1e-139; 1; Mismatches 2;
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; Sequence 7, Application US/09263933; Patent No. 6280940; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HEP FILE REFERENCE: 0125-0005A; CURRENT APPLICATION NUMBER: US/09/263,933; CURRENT APPLICATION NUMBER: 09/129,611; EARLIER APPLICATION NUMBER: 09/129,611; EARLIER FILING DATE: 1998-08-05; NUMBER OF SEQ ID NOS: 33; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 7; LENGTH: 286; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-7
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Sequence 14, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS (FILE REFERENCE: 0125-0005A
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Best Local Similarity
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Pred. No. 7.1e-139;
1; Mismatches 2;
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; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
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US-09-263-933-21
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US-09-263-933-14
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Best Local Similarity
Matches 260; Consert
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Patent No. 62800.
Patent INFORMATION:
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
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Pred. No. 7.1e-139;
1; Mismatches 2;
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Pred. No. 7.1e-139;
1; Mismatches 2;
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US-09-025-769B-265
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ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Es:
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 260; Conserv
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
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APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.(
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                  KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
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Pred. No. 7.1e-139;
1; Mismatches 2;
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US-09-025-769B-362
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; MOLECULE TYPE:
US-09-025-769B-362
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PILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0

PILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEPAX: (212)596-9090

TELEPAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:

TEMORTH- 286 amino acids
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GENERAL INFORMATION:
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Matches
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Best Local Similarity
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
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TYPE: a
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STATE: New York
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l': Moroney, Simon
l': Moroney, Simon
l': Plueckthun, Andreas
INVENTION: Protein/(Poly)peptide libraries
INVENTION: 373
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                                                             KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
                                                                                                                                 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                     KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ
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1251 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09025769B
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Ilag, Vic
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                                                                                                                                                                                                                                                  Score 1330; DB 4;
Pred. No. 7.1e-139;
1; Mismatches 2;
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Americas
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                                                                                                                                                                                                                                                                                     Length 286;
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GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROFILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-08-05

NUMBER OF SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial FEATURE:
OTHER INFORMATION: :
US-09-919-901-7
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US-09-919-901-7
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                                 US-09-919-901-14
                                              RESULT 9
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Best Local Sim:
Matches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09919901 Patent No. 6599738
Sequence 14, Application US/09919901 Patent No. 6599738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 286
TYPE: PRT
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                                                                                                                          SQATMDERNRQIAEIGASLIKHW 263
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Pred. No. 7.1e-139;
1; Mismatches 2;
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GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02

CELL-BASED ASSESSMENT C VIRUS PROTEASE

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US-09-919-901-21
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; OTHER INFORMATION:
US-09-919-901-14
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Best Local Similarity
Matches 260; Conserv
                                                                                      Query Match
Best Local Similarity
                                                                       Matches
                                                                                                                                                                                                                                                              APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 286
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                                                                                                                                                                                             ORGANISM: Artificial
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FNGTH: 286
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                   HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID
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                                                                     Conservative
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                                                                                      98.9<del>%</del>;
                                                                 Score 1330; DB 4;
Pred. No. 7.1e-139;
1; Mismatches 2;
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Pred. No. 7.1e-139;
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RESULT 11
US-09-025-769B-285
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; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik
; APPLICANT: Pack, P
                                                                                                                                                                                            TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 285
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                              Query Match
Best Local Similarity
                                                                                                 Matches
                                                                                                                                                                                                                                                                                                        FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Es
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSEE: James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: N
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  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                 SQATMDERNRQIAEIGASLIKHW 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I James F. Haley, Jr., Esq. 1251 Avenue of the Americas
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                                                                                                 Conservative
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                                                                                                               98.98;
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                                                                                                Score 1330; DB 4;
Pred. No. 7.6e-139;
1; Mismatches 2;
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                                                                                                                             Length 299;
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                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: MORE TELECOMMUNICATION INFORMATION: TELEPHONE: (212)596-9000 TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 298: SEQUENCE CHARACTERISTICS: LENGTH: 299 amino acids
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Patent No.
                                                                                                                         Query Match
Best Local Similarity
Matches 260; Conser
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
AFTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REFERENCE/DOCKET NUMBER: MORPHO/5
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                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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                            AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
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I: USA
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                                                                                                                      98.9%; Score 1330; DB 4; llarity 98.9%; Pred. No. 7.6e-139; Conservative 1; Mismatches 2;
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-300
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US-09-025-769B-300
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Patent No
                                                                                                                                                       Query Match
Best Local Similarity
Matches 260; Consert
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TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/025
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Es
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORP
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
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STATE: New York
COUNTRY: USA
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                                                                                               HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60
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 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKL
                                                      AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNT.
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nilarity 98.9%;
Conservative
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Pack, Pete
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Moroney, Simon
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                                 GRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
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18-FEB-1998
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                                                                                                                                                                 Score 1330; DB 4;
Pred. No. 7.6e-139;
L; Mismatches 2;
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A CURRENT APPLICATION NUMBER: US/09/263,933 CURRENT FILING DATE: 1999-03-08

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

LENGTH: 2307
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US-09-263-933-9
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US-09-263-933-2
; Sequence 2, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:

// TYPE: PRT
// ORGANISM: Artificial Sequence
US-09-263-933-2

Sequence 9, Application US/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
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Best Local Similarity
Matches 260; Conserv
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Pred. No. 1.8e-137;
1; Mismatches 2;
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; ORGANISM: Artificial Sequence
US-09-263-933-9
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SEQ ID NO 9
LENGTH: 2307
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Best Local Similarity 98.9%;
Matches 260; Conservative
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EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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                                                SOATMDERNROIAEIGASLIKHW
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## ALIGNMENTS

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Submitted (APR-1995
[5]
SEQUENCE FROM N.A.
STRAIN=KT1;
MEDLINE=97074643; I
Serebrijski I.G., \(\)
                                                                        SEQUENCE
Kovach M.
                                                                                                                                                                                                                                               Escherichia coli, unidentified, and Alcaligenes hydrogenophilus. Plasmid pJD884, plasmid pRP4 and pBacteria; firmicutes; Bacillales; NCBI_TaxID=1280, 562, 32644, 516;
                                                                                                                                             Needham C., Noble W.C., Submitted (NOV-1995) to [3]
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Q00626; Q57339; C08022; C08102; C09490; C09483; C0939;
C09397; C09398; C09399; C09400; C09401; C09402; C0940;
C09405; C09406; C09407; C09408; C09481; C09482;
C1-NOV-1996 (TrEMBLrel. 01, Created)
C1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
C1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase)
                                                                                                      SEQUENCE FROM N.A.

Maneewannakul K., Maneewannakul S., Ippen-Ihler K.;

Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases
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Submitted (OCT-1995)
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PubMed=8917070;
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SEQUENCE FROM N.A.

MEDLINE=96032859; PubMed=756'
Baron U., Freundlieb S., Gos:
"Co-regulation of two gene ad
bidirectional promoter.";
Nucleic Acids Res. 23:3605-34
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96366236; PubMed=8770413;
Rees S., Coote J., Stables J., Goodson S
Reistronic vector for the creation of
"Bicistronic vector for the creation of
[18]
SEQUENCE FROM N.A.
Schlieper D., von Wil.
Mueller-Hill B.;
Submitted (JAN-1998)
-i- CATALYTIC ACTIVIT
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Lou Y., Holtz A.;
Submitted (FEB-1997)
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Little M., Breitling F.;
Submitted (APR-1997) to
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BioTechniques 20:102-104(1996)
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Storck T., Krueth U., Kolhekar R., Sprengel R., Seeburg P.
"Rapid construction in yeast of complex targeting vectors
manipulation in the mouse.";
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Kitts P.;
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Gossen M., Bujard H.;
"Tight control of gene
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two gene activities by tetracycline
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Yum J.H., Yong D., Shin J.H., Lee K., Chong Y.;

Yum J.H., Yong D., Shin J.H., Lee K., Chong Y.;

"Characterization of a new extended-spectrum beta-lar

"Chong Y.;

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MEDLINE=95172401; PubMed=7867948;
Henrich B., Schmidtberger B.;
"A variant of phiX174 gene E-based posit enhanced lytic potential.";
Gene 154:51-54(1995).

EMBL; Z35638; CAA84692.1; -.
PIR; S47061; S47061.
HSSP; P00810; 1BTL.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001871; Beta_lactamase_A.
Pfam; PF00144; beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE A; 1.
SEQUENCE 286 AA; 31557 MW; 5EB2F2275.
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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Viruses; ssDNA viruses;
NCBI_TaxID=10847;
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RESULT
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 258; Conser
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Best Local S
Matches 258
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99216918; PubMed=10103213;
Arlet G., Goussard S., Courvalin P., Philippon A.,
"Sequence of the genes for TEM-20, TEM-21, TEM-22
spectrum beta-lactamases.";
Antimicrob. Agents Chemother. 43:969-971(1999).
EMBL; Y17581; CAA76793.1; -.
HSSP; P00810; ITEM.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001471; Beta_lactamase.
Pfam; PF00144; beta-lactamase; 1.
PFINTS; PR00118; BLACTAMASEA.
PRINTS; PR00118; BLACTAMASEA.
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Q9R748;
01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=A268; MEDLINE=99216918;
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                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143
                                                                                                                                                                                                      HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60
QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPI
                                                                                                                                                                                                                                                                                                                                                                                                                    PS001
                                                               KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTTPVAMATTLR
                                                                                                                                              AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPAAMATTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTTPVAMATTLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSD
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286 AA;
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98.1%;
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. 20, Last an
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                                          DRWEPELNEATPNDERDT
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Pred. No. 7.8e
3; Mismatches
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Pred. No. 1.1e-103;
2; Mismatches 3;
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7.8e-104;
hes 2;
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                                                                                                                                                  NTAANLLLTTIGGP 120
                                                                                                                                                                                                    FKVLLCGAVLSRVD 83
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OGKPSRIVVIYTTG 240
                                      KLLTGELLTLASRO 203
                                                                                                                                                                                                                                                                                                                                 286;
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                                                               CLITGELLTLASRQ 180
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RESULT
Q8KSD2
AC Q8KSD2
AC Q8
DT 01
DT 01
DT 01
DT 01
DT 01
DT 01
RT B6
OC B6
OC B7
CC B7

RESULT
034176
ID 03
AC 03
DT 01
DT 01
DT 01
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OS KI
OS KI
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                          O34176;
O35, Created)
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O6, Created)
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Best Local S
Matches 257
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Li J.-B., Li X., Yu Y.-S.;

Li J.-B., Li X., Yu Y.-S.;

"Cloning and pronucleus expression of the encoding

"Cloning and pronucleus expression of the encoding

type of beta-lactamases.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ datal

EMBL; AF516720; AAM61953.1; -.

InterPro; IPR001466; Beta_lactamase.

InterPro; IPR001871; Beta_lactamase_A.

Pfam; PF00144; beta-lactamase; 1.

PFam; PF00144; beta-lactamase; 1.

PROSITE; PS00146; BETA_LACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE A; 1.

SEQUENCE 286 AA; 31542 MW; B3DE92C98C5A5EC CR
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Q8KSD2;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
Beta-lactamase TEM-105.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
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  Enterobacteriaceae;
NCBI_TaxID=573;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQATMDERNRQIAEIGASLIKHW
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Pred. No. 2.1e-103;
3; Mismatches 3;
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P. SEQUENCE FROM N.A.

A Yang Y., Bhachech N., Bradford P.A., Jett B.D., Sahm D.F.,

A Yang Y., Bhachech N., Bradford P.A., Jett B.D., Sahm D.F.,

A Yang Y., Bhachech N., Bradford P.A., Jett B.D., Sahm D.F.,

A Yang Y., Bhachech N., Bradford P.A., Jett B.D., Sahm D.F.,

A Yang Y., Bhachech N., Sahm D.F.,

E SEQUENCE 1NCV-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; U95363; AAC32889.2; -.

R HSSP; P00810; 1TEM.

R HSSP; P00810; 1TEM.

R Pfam; PF00144; beta-lactamase; 1.

R Pfam; PF00144; beta-lactamase; 1.

R PRINTS; PR00118; BLACTAMASEA.

R PROSITE; PS00146; BETA LACTAMASE A; 1.

SEQUENCE 286 AA; 31465 MW; 1371745A6119B5B6 CRC64;
Perilli M., Amicosante G.;
"A new TEM ESBL highly active aggregation of the EMBL; Submitted (APR-1999) to the EMBL; EMBL; AF143804; AAF66653.1; -.
HSSP; P00810; 1TEM.
InterPro; IPR001466; Beta_lactam.
InterPro; IPR000871; Beta_lactam.
InterPro; IPR001871; Beta_lactam.
Pfam; PF00144; beta-lactamase; 1
PRINTS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE SEQUENCE 286 AA; 31514 MW; 8
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MEDLINE=98325432; PubMed=9661002;

Yang Y., Bhachech N., Bradford P.A., Jett B.D., Sahm
"Ceftazidime-resistant Klebsiella pneumoniae and Eschisolates producing TEM-10 and TEM-43 beta-lactamases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9LACO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TremBirel.
01-OCT-2000 (TremBirel.
01-MAR-2002 (TremBirel.
Class A beta-lactamase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Enterobacteriaceae; Prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteus mirabilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=584;
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lactamase; 1.
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97.7%;
          TA_LACTAMASE_A; 1.
31514 MW; 8B437C51FC5D60A8
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n St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTGELLTLASRO 203
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Best Local S
Matches 257
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SEQUENCE FROM N.A.

Leflon-Guibout V., Speldooren V., Heym B., Nicolas-Chanoine Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF427127; AAL29433.1; -.

InterPro; IPR001466; Beta_lactamase.

InterPro; IPR000871; Beta_lactamase_A.

Pfam; PF00144; beta-lactamase; 1.

PRINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE A; 1.

SEQUENCE 286 AA; 31483 MW; 582E34D2A08818F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=20448741; PubMed=10991849;

Leflon-Guibout V., Speldooren V., Heym B., Nicolas-
"Epidemiological survey of amoxicillin-clavulanate corresponding molecular mechanisms in Escherichia c France: new genetic features of bla(TEM) genes.";

Antimicrob. Agents Chemother. 44:2709-2714(2000).
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Q93A80;
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                       KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ
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(TrEMBLrel. 23, Last annotation
esistant beta-lactamase TEM-81.
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Pred. No. 2.5e
3; Mismatches
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Pred. No. 2.5e-103;
4; Mismatches 3;
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SEQUENCE FROM N.A.

Hanson N.D., Moland E.S., Pitout J.D.;

"TEM-63, A Novel TEM-type Extended Spectrum Beta-lactama
In Three Different Genera of Enterobacteriaceae from Sou
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

REMBL; AF332513; AAK17194.1; -.

RHSSP; P00810; ITEM.
RINTERPRO; IPR001466; Beta_lactamase.
InterPro; IPR001466; Beta_lactamase_A.

Ffam; PF00144; beta-lactamase; 1.

R PRINTS; PR00118; BIACTAMASEA.

R PRINTS; PR00118; BIACTAMASEA.

R PROSITE; PS00146; BETA_LACTAMASE A; 1.

SEQUENCE 286 AA; 31449 MW; AEBB60086CE3AEB3 CRC64;
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Q9AGJ5;
01-JUN-2001
01-JUN-2001
01-MAR-2002
Extended specations
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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(TrEMBLrel. 17, Last seq
(TrEMBLrel. 20, Last ann
sctrum beta-lactamase TEM
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Pred. No. 2.5e-103;
3; Mismatches 3;
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Q9R435; Q9R435; 01-MAY-2000 (TrEMB) 01-MAY-2000 (TrEMB) 01-OCT-2003 (TrEMB) EXTENDED SPECTRUM ) BLATEM-52. Klebsiella pneumon:

(TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last seq
(TrEMBLrel. 25, Last ann
CTRUM beta-lactamase.

sequence

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286

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RESULT
Q9RMS2
ID Q9
AC Q9
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DT 01
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Matches 257
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EMBL; Y13612; CAA73933.1; -.
PDB; 1HTZ; 21-MAR-01.
GO; GO:0046821; C:extrachromosomal DNA; IE InterPro; IPR001466; Beta_lactamase.
InterPro; IPR0001871; Beta_lactamase_A.
PFANNTS; PR00118; BLACTAMASEA.
PROSITE; PS000146; BETA_LACTAMASE_A; 1.
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"Molecular Evolution c
(ESBL) in Klebsiella F
Submitted (SEP-1997) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Klebsiella.
NCBI_TaxID=573;
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Plasmid.
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SEQUENCE FROM N.A.
STRAIN=KMK107;
                                                                                                                         Q9RMS2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Inhibitor-resistant beta-lactamase TEM-76.
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SEQUENCE FROM N.A.

MEDLINE=20448741; PubMed
Leflon-Guibout V., Speld
"Epidemiological survey
                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                     NCBI_TaxID=562; [1]
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EM865;
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                                                                                                                                                                                                                                                                                                                                QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                                                                                                                                                                                      KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                                                                                                                                                                                      AGQEQLGRRIHYSQNDLVKYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                     AGQEQLGRRIHYSQNDLVEYSPVTEXHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                  QLIDWMEADKVAGPLLRSALPAGWFIADKSGASERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                                                                                                                                                                     KELTAFLHNMGDHVTRLDRWEPELNEAI PNDERDTTTPAAMATTLRKL
                                                                                                                                                                                                                                                               SQATMDERNRQIAEIGASLIKHW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.2%;
larity 97.7%;
Conservative
                                                                                                        coli.
                                                                                                                                                                                                 PRELIMINARY;
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  PubMed=10991849;
Speldooren V., Heym B., Nicolas-Chanoine M.-H.;
survey of amoxicillin-clavulanate resistance and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of blaTEM of Extended Spectrum of k pneumoniae isolated in Korea."; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW;
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Pred. No. 2.5e-103;
3; Mismatches 3;
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beta-lactamase from I
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                                                                                            Enterobacteriales;
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RESULT
Q8KWX4
AC Q8C
DT Q8C
DT Q1
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Best Local S
Matches 257
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Antimicrob. Agents Chemother. 44:2709-2714(2000).

EMBL; AF190694; AAF05613.1; -.

HSSP; P00810; 1XPB.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001871; Beta_lactamase_A.

Pfam; PF00144; beta-lactamase; 1.

PFINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE_A; 1.

SEQUENCE 286 AA; 31485 MW; 63BE4883A7055BD7 CRC6
Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8KMX4;
01-OCT-2002 (TrEMBLrel. 22
01-OCT-2002 (TrEMBLrel. 22
01-JUN-2003 (TrEMBLrel. 24
TEM-93 ES-beta-lactamase.
                                                                                                                                                                                                                                                                                                                                                        Gniadkowski
Submitted (J
[2]
                                                                               "Evolution of TEM extended-spectrum beta-lactamases in F
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ318093; CAC85660.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR000871; Beta_lactamase_A.
Pfam; PF00144; beta-lactamase; 1.
PRONITS; PR00118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
Enterobacteriaceae; Eschei
NCBI_TaxID=562;
                                                                 PROSITE;
Plasmid.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CLSiS 3445/98;
Baraniak A.;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CLSIS 3445/98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Plasmid pblaTEM-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLA-TEM-93
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                                             SEQUENCE
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   Match
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257; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKL
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                                                                                                                                                                                                                                                                                                                                                                               (JUN-2001)
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                                             286
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Escherichia.
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97.7%;
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Pred. No. 2.5e
2; Mismatches
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Last sequence update)
Last annotation update)
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      Score
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      DВ
      2
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      286;
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RESULT
Q8KSD3
ID Q8
AC Q8
DT 011
DT 011
DT 011
DT 011
DT 014
CC Ba
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OC Ba
OC BA
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Best Local S
Matches 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and pronucleus expression of the encoding type of beta-lactamases.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ datal EMBL; AF516719; AAM61952.1; -.
InterPro; IPR001466; Beta-lactamase.
InterPro; IPR000871; Beta-lactamase A.
Pfam; PF00144; beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.
PRINTS; PR00118; BLACTAMASEA; 1.
SEQUENCE 286 AA; 31543 MW; BE679BC8BB18934B CR
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Matches
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Q8KSD3;
01-OCT-2002
01-OCT-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence updat
01-JUN-2003 (TrEMBLrel. 24, Last annotation upo
Beta-lactamase TEM-104.
Klebsiella pneumoniae.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Klebsiella.
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Local Similarity 97.7%;
hes 257; Conservative
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257; Conserv
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A Edelstein M.V.;
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A Edelstein M.V.;
T "Sequence diversity of the genes encoding broad-spectrum TI beta-lactamases in clinical Escherichia coli strains.";
L Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF188199; AAF01046.1; -.
R HSSP; P00810; 1XPB.
R InterPro; IPR001466; Beta_lactamase.
R InterPro; IPR000871; Beta_lactamase_A.
R Pfam; PF00144; beta-lactamase; 1.
R PRINTS; PR00118; BLACTAMASEA.
R PROSITE; PS00146; BETA_LACTAMASE A; 1.
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SEQUENCE 286 AA; 31487 MW; E864BA43B9776ED9 CRC64;
                                             BLA TEM-17.
Capnocytophaga ochracea.
Bacteria; Bacteroidetes; Flavobacte
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Quentin R.;

"Capnocytophaga ochracea: characterization of a plasmid-encoded
extended-spectrum TEM-17 beta-lactamase in the phylum Flavobacter-
Bacteroides.";

Antimicrob. Agents Chemother. 44:760-762(2000).

R EMBL; Y14574; CAA74912.2; -.

R HSSP; P00810; 1XPB.
InterPro; IPR001466; Beta_lactamase.
InterPro; IPR001871; Beta_lactamase.

R Ffam; PF00144; beta-lactamase; 1.
PFam; PF00114; beta-lactamase; 1.
PRINTS; PR00118; BLACTAMASEA.

PRINTS; PR00118; BLACTAMASEA.

PROSITE; PS00146; BETA_LACTAMASE_A; 1.

SEQUENCE 286 AA; 31514 MW; BD498F6B9D369345 CRC64;
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22	u	. 00	N	N	89	681
2.3	(L	. &	0	σ	598	981
24	w	8	æ	σ	ADA67747	57747 Beta-la
25	Û	8	œ	N	AAR88636	88636 Plasmid

PR XX PR

13-JAN-2000; 2000US-0175968P. 15-MAR-2000; 2000US-00526106.

16-JAN-2001; 2001WO-US001651.

19-JUL-2001.

## ALIGNMENTS

RESULT 1
AAE05544
ID AAE0
XX
AC AAE0
XX
DT 24-S
XX
DE E. c
XX
XX
DE Minte
KW Circ
KW type

24-SEP-2001

(first entry)

AAE05544;

E. coli mature TEM-1 beta-lactamase.

AAE05544 standard; protein; 263

ΑA

KW	Interaction-dependent	endent enzyme association; IdEA system; biosensor;
XW	circularly perm	circularly permutated interaction-activated protein; marker protein;
3	type A beta-lac	type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;
公	therapeutic; dr	therapeutic; drug screening; thioredoxin; ampicillin resistance.
X		
SO	Escherichia coli	•
X		
H	Key	Location/Qualifiers
FΤ	Cleavage-site	2728
FT		<pre>/note= "Break-point between alpha and omega fragments"</pre>
ΗT	Region	ţ
ΗΉ		/note= "Inter-sub-domain loop"
ΉŢ	Cleavage-site	3839
H		<pre>/note= "Break-point between alpha and omega fragments"</pre>
ΉŢ	Active-site	45
ΗŢ	Cleavage-site	7475
ΗŢ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
Η̈́	Cleavage-site	
ΉŢ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
Ή	Cleavage-site	9
FT		<pre>/note= "Break-point between alpha and omega fragments"</pre>
Į	Region	189 204
FT		/note= "Inter-sub-domain loop"
FΤ	Cleavage-site	190191
FΤ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
FΤ	Cleavage-site	i
FΤ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
ΉŢ	Cleavage-site	(
ΉŢ		<pre>/note= "Break-point between alpha and omega fragments"</pre>
×		ı
PN	WO200151629-A2.	
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The marker protein is preferably a type A beta-lactamase, especially TEM-CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a CC proteome library selected from single chain antibody Fv fragment library, CC an antibody light chain variable region library and a peptide library, CC displayed within thioredoxin. The IdEA systems are useful for detecting and identifying interactions between intracellular as well as CC extracellular proteins, particularly between two or three polypeptides. CC incorporation of multiple genetic traits in a host cell. In particular, CC the systems are also useful in many applications in human therapeutics, compositics and prognostics, as well as in high-throughput screening compositive and prognostics, as well as in high-throughput screening compositive systems (e.g. E. coli Dimer Detection System, yeast two-dried system or Selective Infective Phage System) require multiple steps and compositive and phenotype, which cause severe loss of efficiency compositive and false negative rates. The present system compositive and the service in a high throughput format. The circularly permutated marker proteins comprising interaction-dependent enzymes find use in cell-based sensors for activation or compositive and in cell-based sensors for activation or compositive and in cell-based sensors for activation and between the proteomes of cells, tissues and pathogenic organisms, and in compositive and in the present sequence is Escherichia coli mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-declining alpha-decay and mu
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Best Local S
Matches 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   form functionally reconstituted marker proteins which produce a detectable signal upon the association of two oligopeptides, or upon simultaneous association of two oligopeptides with a third oligopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interaction-dependent enzyme association systems for detecting interactions between two or three polypeptides, especially in human therapeutics, diagnostics or prognostics, comprise circularly permutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-451857/48.
N-PSDB; AAD10411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Balint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IdEA) systems that concircularly permutated,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-protein interaction. The pres
mature TEM-1 beta-lactamase enzyme fi
lactamase is a product of ampicillin
domains, alpha-omega and mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PANO-) PANORAMA RES
                                                                                                                               121
                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                               260;
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                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                              KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLIGELLTLASRQ
                                                                                                                                                                                                                                           AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                          HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
SQATMDERNRQIAEIGASLIKHW 263
                                                                QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                               KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGE
                                          QLIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to new interaction-dependent encyme action sequence that encodes for a mutated, interaction-activated proteins that reassemble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC
                                                                                                                                                                                                                                                                                                                                                                                                                  98.9%;
                                                                                                                                                                                                                                                                                                                                                                                          Score 1330; DB 4;
Pred. No. 1.9e-129;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a fragment complementation system (I) which comprises a first oligopeptide (OP1) containing an N-terminal CC fragment with a C-terminal break point and a second oligopeptide (OP2) fragment with a C-terminal break point and a second oligopeptide (OP2) CC comprising a C-terminal with a N-terminal breakpoint, in which the C and CC neassemble to form a functionally reconstituted MP. Methods from the CC present invention are used for monitoring the occurrence of protein (MP) and CC protein interactions in a sample, identifying oligopeptide interactions CC protein interactions in a sample, identifying epitopes that bind to an CC between two different proteomes, identifying epitopes that bind to an immunoglobulin (Ig) variable region, for identifying interactions between extracellular domain of a transmembrane protein and a polypeptide, for high-throughput identification of compounds that inhibit phosphorylation-cc regulated signal transducers, forming a enzyme complementation system for selecting simultaneous in need of it. The present sequence represents
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                               Matches
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13-JAN-2000; 2000US-0175968P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel fragment complementation system polypeptides comprises fragment pairs that reassemble into a marker protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-032034/04
N-PSDB; AAC90773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  host cell and for activating a beta-lactam derivative of compound in a host who is in need of it. The present sequence the Escherichia coli mature TEM-1 beta-lactamase, which exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                  260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                263
AGQEQLGRRIHYSQNDLVBYSPVTEKHLTDGMTVRELCSAAITMSDNT
                                                                                                    HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTEF
                                                                                                                                                             HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFK
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; 94pp; English.
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                                                                                                                                                                                                                                                                                                        98.9%;
98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                                                  Score 1330; DB 4;
Pred. No. 1.9e-129;
l; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-lactamase protein sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment complementation system ide (OP1) containing an N-termin point and a second oligopeptide point and a second oligopeptide in which the containers of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to identify interact
having first and see
which has a directl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rst and second members a directly detectable
                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                         Indels
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                                                                                                                 CVLLCGAVLSRID
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N-terminal
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AANLLLTTIGGP 120
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AANLLITTIGGP 120

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                                       Query Match
Best Local Sim
Matches 260;
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                                                                                                             Escherichia coli beta-lactamase (AAW16634), including the signal peptide is the expression product of a molecular chimaera, designated pCMV-BL (AAT66737), in which the beta-lactamase gene is under control of the CMV intermediate/early promoter. Vectors consisting of a transcriptional regulatory DNA sequence linked to a beta-lactamase gene can be used for enzyme prodrug therapy. Expression of the beta-lactamase in a targetted cell allows conversion of a prodrug into an agent toxic to the cell for treatment of cancer, viral (e.g. HIV) infection or inflammation. Secretion of the enzyme has the advantage of increasing neighbouring cel
                                                                                     Sequence
                                                                                                                                                                                                                                                       Molecular chimaera for gene or virus directed enzyme prodrug therapy useful for treatment of cancer, viral infection or inflammation.
                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1996;
                                                                                                                                                                                                                                       Example;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directed enzyme
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)B; AAT66736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directed enzinflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                     98.9%;
Similarity 98.9%;
50; Conservative
                                                                                                                                                                                                                                                                                                                                 Moore
                                                                                                                                                                                                                                                                                                                                                         GLAXO
HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID
                                                                                     264
                                                                                                                                                                                                                                      Page 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQATMDERNRQIAEIGASLIKHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prodrug therapy; GDEPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prodrug therapy;
                                                                                                                                                                                                                                    English.
                                   Score 1330; DB 2;
Pred. No. 1.9e-129;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDEPT; beta-lactamase;
                                                          Length
                                     Indels
                                                            264;
                                   ٠<u>.</u>
                                                                                                                                                                                     gnal peptide,
d pCMV-BL
l of the CMV
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                                  Gaps
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RESULT 4
AAW18680
ID AAW1
XX
AA AAW1
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DT 13-A
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DE Intr
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DE Intr
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DE Sech
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CS Esch
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PN WO97
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PP 10-N
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PP 10-N
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CG List
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
Query Match 98.9
Best Local Similarity 98.9
Matches 260; Conservative
                                                                                            The intracellular form (AAW18680) of TEM beta-lactamase pCMV-delBL (AAT70311) in which a PCR-amplified beta-lact sequence, minus the signal sequence, is placed under cor intermediate/early promoter of cytomegalovirus. Intracel lactamase constructs, placed under control of promoter/e of lung-associated protein or neuroendocrine marker prot used in novel chimaeric molecules for use in prodrug the
                                                        Sequence
                                                                                                                                                                                                                             DNA construct for gene-directed enzyme prodrug therapy comprises lung- or neuroendocrine-specific promoter contexpression of prodrug-converting enzyme.
                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                   Dev I,
                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodrug therapy; virus directed en
                                                                                                                                                                                                                                                                                                                                                              (GLAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9719183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-lactamase; pCMV-delBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intracellularly-expressed beta-lactamase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW18680;
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                                                                                                                                                                                                         8iii; Page 32-34;
                                                                                                                                                                                                                                                                                                                                   Moore
                                                                                                                                                                                                                                                                                                                                                              GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQATMDERNRQIAEIGASLIKHW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                       AA;
                                                                                                                                                                                                                                                                                                                                  JT,
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                                                                                                                                                                                                                                                                                                                                                             GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y; gene
enzyme
                                                                                                                                                                                                                                                                                                                                                                                       95GB-00023703
                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-GB002846
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                                                                                                                                                                                                                                                                                                                                   Sethna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
             98.9<del>%;</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prodrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         directed
                                                                                                                                                                                                         53pp; English.
                                                                                                                                                                                                                                                                                                                                   ; ad
Score 1330; D
Pred: No. 1.9e
1; Mismatches
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therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prodrug;
DB 2;
..9e-129;
les 2;
                                                                                           promoter/enhancer elements marker protein genes, can be prodrug therapy of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy;
lung can
                       Length
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                                                                                                                                                                                                                                             of lung cancer
strolling
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er;
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                           264;
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                                                                                                                                                                          is expressed by
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYP1A1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-2003
04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR31575;
                                                                             but were constructed using different strategies (see AAQ36498). The constructs comprise exons 2-7 of human CYP1A1 gene under the control of the inducible mouse metallothionein (MMT-1) promoter. The constructs also contain an open reading frame in the opposite orientation to the cytochrome P450 exons. This ORF encodes ampicillin resistance. The constructs are suitable for transformation of human fibroblasts derived from the xeroderma pigmentosum group A. Cultures of the transformed fibroblasts can be used to test substances for mutagenicity. The presence of the inducible cytochrome P450 gene allows metabolism of the substance to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                 The expression constructs pRNH127 and pRNH155 contain identical sequences but were constructed using different strategies (see AAQ36498). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     In vitro method for testing mutagenicity of a chemical - by met-
chemical cell line consisting of transformed fibroblasts having
detectable cytochrome P450 mixed function oxidase activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                        to mutagenic field.)
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Query Match

86

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Score

1330;

B <u>ب</u>

Length 286;

286

Sequence

286

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene therapy; gene directed enzyme prodrug therapy; GDEPT virus directed enzyme prodrug therapy; VDEPT; prodrug act. cytotoxic; cytostatic; cancer; tumour; retrovirus; vector beta-lactamase; cephalosporin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-1996
                                                                       A secretory beta-lactamase (AAR97619) is expressed from DN pCMV-BL (AAT29220), in which the beta-lactamase coding sequence the control of the intermediate/early cytomegalovirus promulactamase delivery to mammalian cells confers sensitivity cephalosporin prodrugs. Liposomal DNA/5-fluorouracil prodrugsulted in s.c. tumour regression in mice bearing A549 to of mice bearing human large cell lung H460 intrathoracic was increased upon i.t. injection of the secretory beta-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                          Molecular chimaera for use in enzyme gene therapy - is a target cell to express a secretable enzyme which cleaves outside the cell into a cytotoxic or cytostatic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-1994;
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                                                                                                                                                                                                                                                                                                            3; Page 57-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT29220.
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L; Mismatches 2;
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(i.t.) tumours
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Best Local S
Matches 260
The present sequence is encoded by a chimeric mouse metallothionein-cytochrome P450IA1 (CYPIA1) expression construct. Two clones, pRNH127 and pRNH15, were isolated by different methods and which both had the same sequence. The CYPIA1 construct is used in assays to test for cytotoxicity of humans to a chemical. The method comprises exposing human fibroblast cells normally not including any cytochrome P450 activity to potentially toxic chemicals. The cells having been transformed to express cytochrome P450, under the control of a controllable promoter through the CYPIA1 gene, upon exposure to the chemical in vitro. The chemical is metabolised
                                                                                                                                       Testing chemicals for cytotoxicity to human by using recombinant fibroblasts transformed with control of inducible promoter.
                                                                                                                                                                                        WPI; 1996-286397/29.
N-PSDB; AAT30354.
                                                                                                                     Disclosure; Col
                                                                                                                                                                                                                                                                      27-JUN-1991;
09-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome; metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome
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25-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
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92US-00990295
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Pred. No. 2.2e-129;
L; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                            mouse;
                                                                                                                                                                                                                                                                                                                                                                                                            human;
                                                                                                                                                   detecting gene of cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxicity; assay;
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RESULT 8
AAW16635
ID AAW1
XX AAW1
AC AAW1
XX O9-A
XX Beta
XX Gene
KW Gene
KW HIV;
XX Escl
XX V1:1
YN WO97
XX O9-A
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XX U9
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Best Loc
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                                                                                              Example;
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                                                                                                                             chimaera for gene or virus or treatment of cancer, viral
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Pred. No. 2
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                                                                                                                              directed enzyme prodrug therapy infection or inflammation.
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2.2e-129;
hes 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-lact
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Escherichia coli beta-lactamase (AAW16639 is the expression product of a molecular (AAT66738), in which the beta-lactamase content intermediate/early promoter. Vectors content

e (AAW16635), Lac...
e molecular chimaera, des...
ractamase gene is under c

y the signal peptide, designated pCMV-delBL ler control of the CMV a transcriptional

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RESULT 9
AAW18679
ID AAW1
XX
AAW1
AC AAW1
XX
DT 13-A
XX
DE Secr
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CW Proc
KW Proc
KW Proc
KW Proc
FT Prot
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SX

ESCh
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COMP
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Matches 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the cell for inflammation
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                                                                                              WPI; 199
N-PSDB;
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DNA construct for gene-directed enzyme prodrug therapy of lung cancer comprises lung- or neuroendocrine-specific promoter controlling expression of prodrug-converting enzyme.
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                                                                                                                                                                                                                                                      20-NOV-1995;
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DB; AAT70309.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                            GROUP
                                                                                                                                                                                                                                                      95GB-00023703
                                                                                                                                                                                                                                                                                                   96WO-GB002846
                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .23
/label= Sig_peptide
24. .286
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                 Sethna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                             LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.98;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mat_protein
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Pred. No. 2.2e-129;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prodrug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSAAITMSDNTAANLLLTTIGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDEPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
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RESULT 10
AAY08529
ID AAY08
XX AAY08
AC AAY08
XX O3-AL
DT O3-AL
XX Vecto
XX Firef
KW Firef
KW insec
KW insec
KW insec
XX Synth
XX Synth
XX AC
PN WO99;
XX AC
PN WO99;
XX AC
PF 11-NC
XX AC
XX AC
PF 11-NC
XX AC
XX AC
PF 11-NC
XX AC
PF
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Best Local S
Matches 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Firefly; luciferase; tetracycline; tr
tetracycline repressor; tetracycline
insect; Tn10; medicine; dosage; chees
allergy.
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector pASK75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-1999
                                            N-PSDB;
                                                                                                                                                 (KORP/)
(KARP/)
(KURI/)
                                                                                                                                                                                                                                   14-NOV-1997;
                                                                                                                                                                                                                                                                        11-NOV-1998;
                                                                                                                                                                                                                                                                                                                 27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                            WO9925866-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Sim
                                                                                                        Korpela
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                                            1999-338015/28
DB; AAV72418.
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                                                                                                                                               KORPELA M.
KARP M.
KURITTU J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bii;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQATMDERNRQIAEIGASLIKHW
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                                                                                                        Karp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
    tetracycline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-la protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JGRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.9%;
                                                                                                           Kuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1330; D. Pred. No. 2.2e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ne; transcriptional control; TetR; TetA; sline promoter; luminescence; luxCDABE; cheese production; antibiotic; foodstuff;
        recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286
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.2e-129;
.es 2;
        prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AANLLLTTIGGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86;
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ing sequence is
           cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AANLLLTTIGGP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /LLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein or chimaeric
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using

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RESULT 11
AAB10442
ID AAB10
XX
AC AAB10
XX
DT 01-DE
XX
DE Expre
XX
CW Expre
KW Expre
KW Blyn
XX
OS Synth
XX
PN DE199
XX
PD 13-J1
XX
PF 11-J1
XX
PR 11-J1
XX
PR 11-J1
XX
PA (DEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Д
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel tetracycline assay that uses recombinant prokaryotic cells comprising a luciferase gene under the transcriptional control of a tetracycline repressor and tetracycline promoter and control of a tetracycline repressor and tetracycline promoter and converse the detection of luminescence emitted form the cells. The assay can be used to distinguish tetracycline form other microbial agents. The convention also describes a novel plasmid comprising either the luxCDABE genes, a tetracycline repressor (TetR) and a tetracycline promoter (TetA) from Tn10. The tetracycline assay convention at the tetracycline assay to study the dosage and penetration of the medicine. The method can also be used to test cheese production, as cheese making bacteria are not also be used to test cheese production, as cheese making bacteria are not determine the presence of tetracycline. The method can also be used to determine the presence or concentration of antibiotics in foodstuffs, c.g. for allergic people. The present assay method does not rely on the present assay is also more sensitive, as even a small amount of liminescence can be also more sensitive, as even a small amount of antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 260
                                 11-JAN-1999;
                                                                 11-JAN-1999;
                                                                                                                                 DE19900635-A1
                                                                                                                                                                                                   Expression vector; antibody
B lymphocyte; myeloma cell;
                                                                                                  13-JUL-2000
                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                    Expression
                                                                                                                                                                                                                                                                                   01-DEC-2000
                                                                                                                                                                                                                                                                                                                    AAB10442;
                                                                                                                                                                                                                                                                                                                                                  AAB10442 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
  (DEKR-) DEUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luminescence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPETLVKVKDAEDQLGARVGYTELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
                                                                                                                                                                                                                                                                                                                                                                                                                                      SQATMDERNRQIAEIGASLIKHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQATMDERNRQIAEIGASLIKHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KELTAFIHNMGDHVTRLDRWEPELNEAI PNDERDTTMPVAMATTLRKLLTGELLTLASRQ
                                                                                                                                                                                                                                                vector pSEX15G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 47-48; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can
  KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                (first entry)
                                  99DE-01000635
                                                                 99DE-01000635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.9%;
                                                                                                                                                                                                                                                bla protein.
                                                                                                                                                                                               binding protein; monoclonal antibody; Neo-R; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                   286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1330; D
Pred. No. 2.2e
1; Mismatches
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Query Match Best Local (

Similarity

98.9%;

Length

286;

Sequence 286

AA;

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This invention describes a novel method for the selection of monoclonal call antibodies (MAD) which comprises (i) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas such that the antibodies are presented at the surface of the hybridomas by an antibody-binding CC protein (I); and (ii) binding the antibody to antigens (Ag). The cinvention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) cc molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select MAD with specificity for particular antigens. MAD can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally on the basis of strength of affinity for a particular antigen. Complex constitutes of hybridomas can be used for selection, reducing the time and cost involved in MAD selection. This sequence represents the bla protein contained in the expression vector pSEX15G2 which contains the CC bla protein, Neo-R and protein G described in the method of the invention
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N-PSDB; AAA71430.
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Expression

vector pSEX11L4 bla protein

Expression vec B lymphocyte; vector; antibody binding protein; monoclonal oma cell; hybridoma; protein G; bla p rotein. antibody; Neo-R;

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AAB10440
ID AAB1
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Pred. No. 2.2e-129;
1; Mismatches 2;
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Pred. No. 2.2e-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide encoding a polysaccharase under the transcriptional control of a surrogate promoter capable of increasing expression of the polysaccharase. The host cell also contains a second heterologous polynucleotide encoding a secretory polypeptide to facilitate the secretion of the expressed polysaccharase. The recombinant host cell is useful for producing polysaccharase which is useful for enzymatically degrading oligosaccharides such as lignocellulose, hemicellulose, cellulose, pectin or their combinations, and fermenting the product to ethanol, by simultaneous saccharification and fermentation processes. The present sequence is encoded by an integration vector which was introduced into cells to generate recombinant host cells. The vector contains a surrogate promoter from Zymomonas mobilis, the celZ gene from Erwinia chrysanthemi, resistance markers bla and tet, and Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                           Sequence
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N-PSDB; AAC91455.
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                                                                                                                                                         HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID
KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ
                                                                                            AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP
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|llarity 98.9%;
|Conservative
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                                                                                                                                                                                                                                                            Score 1330; DB 4;
Pred. No. 2.2e-129;
1; Mismatches 2;
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Similarity

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      Query Match
Best Local S
Matches 260
                                                                                                                                                             present plasmid in the m
                                                                                                                                                                           The specification describes a method for assessing the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The method comprises introducing at least two reporter genes encoding luminescent and/or fluorescent products into the micro-organisms, incubating the micro-organism within the desired environment, and detecting luminescence and/or fluorescence after a predetermined time period. Use of two different markers within a micro-organism enables the differentiation between growth and death rates. The method is used to assess the growth rate and death rate of a micro-organism within a predetermined time period in a desired environment. The present sequence represents a beta-lactamate protein, and is encoded by a plasmid which encodes luminescent and fluorescent proteins, and is used in the method of the invention
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assessing growth and death rates of a micro-organism in a deenvironment, by introducing 2 reporter genes encoding lumine fluorescent products and detecting luminescent fluorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 28-29; 32pp;
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Searc Job t	DЬ	Ϋ́Ο	da	Qγ	Дb	VQ.	dd	γQ
Search completed: June 18, 2004, 19:08:00 Job time : 63 secs	264 SQATMDERNRQIAEIGASLIKHW 286	241 SQATMDERNRQIAEIGASLIKHW 263	204 QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 263	181 QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240	144 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQ 203	121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180	84 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143	61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120

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Result
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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US-09-490-324-362
US-10-416-708A-73
US-10-045-674A-523
US-10-045-674A-523
US-09-490-324-298
US-09-490-324-300
US-10-668-035-57
US-10-622-088-114
US-10-491-653-146
US-10-491-653-146
US-10-414-532-65
US-10-453-372-332
US-10-414-532-333
US-10-414-532-38
US-10-414-532-28
PCT-US04-12717-118
US-10-831-070-118
US-60-556-841-6264
US-10-796-280-761
US-10-474-792-90
US-60-556-841-406
PCT-US04-02188-101
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Sequence 265, App
Sequence 362, App
Sequence 73, Appl
Sequence 285, App
Sequence 298, App
Sequence 300, App
Sequence 9, Appli
Sequence 114, App
Sequence 6154, App
Sequence 65, Appl
Sequence 65, Appl
Sequence 33, Appli
Sequence 28, Appli
Sequence 118, App
Sequence 118, App
Sequence 58, Appli
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Sequence 58, Appli
Sequence 6264, App
Sequence 3455, Ap
Sequence 3455, Ap
Sequence 90, Appl
Sequence 90, Appl
Sequence 406, App
Sequence 406, App
Sequence 406, App
Sequence 406, App
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equence 220, A	equence 3	equence 1221	equence 37,	equence	equence	19522	equence 294.	equence 3776.		equence 2583.	190.	e 456	e 11741.		equence 390,	equence	equence 4337.	

## ALIGNMENTS

Application US/09490324

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; MOLECULE SEQUENCE US-09-490-324-265
                                                                                                          NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEPHONE: (212)596-9090
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
Query Match
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Tames F Waller: IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & N
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                   TYPE: amino acid
                                                                TOPOLOGY: linear ULE TYPE: protein
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                                                  TYPE: protein DESCRIPTION: |
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Ilag, Vic
Ge, Liming
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                                                SEQ ID
                                                  NO:
                                                265:
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US-09-490-324-362
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                              ; MOLECULE SEQUENCE US-09-490-324-362
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Matches
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GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Query Match
                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 362:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                           APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
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ADDRESSEE: James F.
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                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1251 Avenue
                                                 TOPOLOGY: linear ULE TYPE: protein CESCRIPTION:
                                                                                                    TYPE: amino acid
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RESULT 3
US-10-416-708A-73
US-10-416-708A-73
; Sequence 73, Application US/10416708A
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja
; TITLE OF INVENTION: CREATION AND IDENTIFICATI
; TITLE OF INVENTION: SPECIFICITIES
; TITLE OF INVENTION SPECIFICITIES
; FILE REFERENCE: 37779-0004
; CURRENT APPLICATION NUMBER: US/10/416,708A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 73
; LENGTH: 286
RESULT 4
US-10-045-674A-523
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGK
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                                                                                                 SQATMDERNRQIAEIGASLIKHW 263
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                                                                               SQATMDERNRQIAEIGASLIKHW
                                                                                                                                                                                                                                                                                                                                                                   98.9%;
llarity 98.9%;
Conservative
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1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                    Score 1330; DB 6;
Pred. No. 1.7e-119;
1; Mismatches 2;
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Application

US/10045674A

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RESULT 5
US-09-490-324-285
US-09-490-324-285
; Sequence 285, Applicatio
; GENERAL INFORMATION:
APPLICANT: Knapp
APPLICANT: Knapp
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TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING

TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY

TITLE OF INVENTION: LIBRARIES

FILE REFERENCE: DYAX/002 CIP2

CURRENT APPLICATION NUMBER: US/10/045,674A

CURRENT FILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: 06/198,069

PRIOR APPLICATION NUMBER: 09/837,306

PRIOR APPLICATION NUMBER: 09/837,306

PRIOR FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 635

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 523

LENGTH: 286
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Best Local Similarity 98.9
Matches 260; Conservative
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                                             Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq. c/o Fish & STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
HOET, RENE
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CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                               SQATMDERNRQIAEIGASLIKHW 263
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Ilag, Vic
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Pred. No. 1.7e-119
1; Mismatches 2
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RESULT 6
US-09-490-324-298
US-09-490-324-298, Application US/v>...; Sequence 298, Application US/v>...; GENERAL INFORMATION:
APPLICANT: Knappik, Achim Pack, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: 9
US-09-490-324-285
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TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
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                                                           NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Innressee: James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                      TITLE OF
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STREET: 1251 Avenue of CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                             Moroney, Simon
Plueckthun, Andreas
OF INVENTION: Protein/(Poly)peptide
OF SEQUENCES: 373
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Ilag, v.
~e, Liming
~v, Simon
And
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of the
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Pred. No. 1.9e-119;
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US-09-490-324-300
; Sequence 300, Applicat:
; GENERAL INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 298:
US-09-490-324-298
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REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 298:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EPB-1998
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
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nes 260; Conservative
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                                                Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                             APPLICANT: Knappik,
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                CITY: New York
STATE: New York
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COUNTRY: USA
                                                                                                                                                                                                                                                                                    Application US/09490324
                                                                                                                                                                                                        Pack, Pete
Ilag, Vic
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98.9%;
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Sequence 9, Application US/10842534; GENERAL INFORMATION:

APPLICANT: Stewart, Francis

APPLICANT: Zhang, Youming

APPLICANT: Zhang, Youming

APPLICANT: Buchholz, Frank

TITLE OF INVENTION: NOVEL DNA CLONING METHOD

FILE REFERENCE: 2923-618

CURRENT FILING DATE: 2004-05-11

PRIOR APPLICATION NUMBER: US/10/842,534

CURRENT FILING DATE: 2002-08-30

PRIOR FILING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: US 09/555,510

PRIOR APPLICATION NUMBER: PST/55,510

PRIOR APPLICATION NUMBER: PST/598/07945

PRIOR APPLICATION NUMBER: PST/11NG DATE: 1908-12-05

PRIOR APPLICATION NUMBER: EP 97121462.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: US-09-490-324-300
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US-10-842-534-9
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FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 260; Conser
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240
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Pred. No. 1.9e-119;
L; Mismatches 2;
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; LENGTH: 1293
; TYPE: PRT
; ORGANISM: Homo s
US-10-668-035-57
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; NAME/KEY: DOMAIN
; LOCATION: (1)..(286)
; OTHER INFORMATION: bla g
US-10-842-534-9
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US-10-668-035-57
; Sequence 57, Applica; GENERAL INFORMATION:
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; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
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    Query Match
Best Local Similarity
Matches 259; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek APPLICANT: Liaw, Chen W. APPLICANT: Lin, I-Lin APPLICANT: Lowitz, Kevin P. APPLICANT: Lowitz, Kevin P.
                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lowitz, Kevin P.
APPLICANT: Chen, Ruoping
TITLE OF INVENTION: Endogenous, Constitutively
TITLE OF INVENTION: Orphan Receptors
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ע ID NO 57
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                                                                                                                                                           version 3.1
                   98.5%;
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Score 1329; DB 6;
Pred. No. 1.8e-118;
2; Mismatches 2;
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Pred. No. 2.2e-119;
2; Mismatches 2;
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                                   Length 1293;
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8 8 8

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61 63

AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120

KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180

CLITGELLTLASRO 182

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                                     Qy
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APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR FILING DATE: 2003-03-04
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
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                                                                           Query Match
Best Local S
Matches 258
                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                        ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                              : Edal
                                                                                                                                                                                                                                              LENGTH:
                                                                          Local Similarity
tes 258; Conserv
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KELTAFLHNMGDHVTRLDRWBPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 484
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                                                                           Conservative
                                                                                                                                                                   Amino acid sequence
                                                                                          98.0%;
98.1%;
                                                                                            Score 1318; DB 6;
Pred. No. 2.2e-118;
                                                                           Mismatches
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                                                                                                         Length
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                                                                                                                265;
                                                                         0; Gaps
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CURRENT FILING DATE:

2003-12-01

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; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-491-653-146
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US-10-491-653-146
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US-10-724-972A-6154
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APPLICANT: Kuhlwein, Thorsten
APPLICANT: Luttgau, Sandra
TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins
FILE OF INVENTION: From Said Libraries
FILE REFERENCE: 4121-162
CURRENT APPLICATION NUMBER: US/10/491,653
CURRENT FILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: EP 01123596.7
PRIOR APPLICATION NUMBER: EP 01123596.7
PRIOR APPLICATION NUMBER: PCT/EP02/10852
PRIOR APPLICATION NUMBER: PCT/EP02/10852
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 151
SOFTWARE: PatentIn version 3.2
SEQ ID NO 146
LENGTH: 498
Sequence 6154, Application US/10724972A
GENERAL INFORMATION:
APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNO
FILE REFERENCE: PATH03-16
CURRENT APPLICATION NUMBER: US/10/724,972A
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Best Local Similarity
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                  ATMDERNRQIAEIGASLIKHW
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98.5%;
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Pred. No. 1.8e-116;
1; Mismatches 3;
                                                                                                                                                                                                                                                                              263
                                                                                                                                                                                                                                         498
                                          AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 498;
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PRIOR APPLICATION NUMBER: 09/450,969
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO 6154
LENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-10-414-532-65
; Sequence 65, Application US/10414532
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
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                                                                                                                                          US-10-414-532-65
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VA-
TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
FILE REFERENCE: 56029-40437
CURRENT APPLICATION NUMBER: US/10/414,532
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: 60/372,710
PRIOR FILING DATE: 2002-04-16
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 65
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Best Local Similarity
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                                                                                                       Query Match
                                                                                                                                                        OTHER INFORMATION: Description OTHER INFORMATION: sequence of OTHER INFORMATION: pYA3637
                                                                                                                                                                                                           LENGTH: 290
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
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                                                                                      Similarity
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HPETLVKVKDAEDQLGA--RVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSR 58
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                                                                      13.0%;
larity 24.1%;
Conservative 38
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                                                                      Score 175; DB 6; 1
Pred. No. 6.7e-09;
8; Mismatches 101;
                                                                                                                                                                            of Artificial Sequence: Protein blaSS-pspA-EF5668-bla C-term region in
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                                                                                                       Length 290;
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                                                                      100; Gaps 10;
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; TYPE: PRT
; ORGANISM: Homo
US-10-453-372-332
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US-10-453-372-332
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 332
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                                                                                                              Matches
                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
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CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alsobrook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/208263
FILING DATE: 2000-05-21
APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/195792
FILING DATE: 2000-03-10
APPLICATION NUMBER: 09/839446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/823187 FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/185967 FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/199476
FILING DATE: 2000-03-25
APPLICATION NUMBER: 09/863776
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                         63
                                                                                                                          Similarity
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                                                                     ETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRIDAG
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6; Mismatches 10
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GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACI
FILE REFERENCE: 21402-589 A
                                                                                                                                   Matches
                                                                                                                                                   Query Match
Best Local Similarity
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Remaining Prior Application
NUMBER OF SEQ ID NOS: 1609
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CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
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TH: 841
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FILING DATE: 2001-03-29
FILING DATE: 2001-03-29
APPLICATION NUMBER: 60/195792
FILING DATE: 2000-03-10
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APPLICATION NUMBER: 09/939398
FILING DATE: 2001-08-24
APPLICATION NUMBER: 60/227800
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APPLICATION NUMBER: 60/185967
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APPLICATION NUMBER: 09/863776
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2003-06-03
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5; Mismatches 10
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